



APPLICATION
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TITLE OF THE INVENTION:

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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *M. CATARRHALIS*
FOR DIAGNOSTICS AND THERAPEUTICS

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RELATED APPLICATIONS:

This application claims the benefit of U.S. Provisional Application Serial Number
60/128,476, filed April 9, 1999, the entire teachings of which are incorporated herein by
reference.

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BACKGROUND OF THE INVENTION

The genus *Moraxella* is a member of the family *Neisseriaceae*. The 10 species of this genus are separated into 2 subgenera, *Moraxella* (rods) and *Branhamella* (cocci). *Moraxella* are gram-negative, aerobic, oxidase-positive, and usually catalase-positive. (Bovre, K. 1984. Genus II. *Moraxella* Lwoff 1939, 173 emend. Henriksen and Bovre 1968, 391, 105. Krieg and Holt (editors) In Bergey's Manual of Systematic Bacteriology, 1:296-303.). *Moraxella catarrhalis*, a member of the subgenera *Branhamella*, was previously called *Branhamella catarrhalis* and *Neisseria catarrhalis*.

Moraxella catarrhalis is frequently isolated from the nasal cavity of humans, and until recently, was considered a nonpathogenic commensal of the upper respiratory tract. Currently it is most important lower respiratory pathogen after *S.pneumoniae* and *H. influenzae* (Doren, G., et al, 1986. Diagn. Microbiol. Infect. Dis. 4:191-201.). It is a common cause of otitis media in children, acute bronchitis or pneumonia in adults, and sinusitis (Wood, G., et al, 1996. Clin. Infect. Dis. 22:632-636.). Bacteremia, meningitis, skeletal infections and endocarditis due to *M. catarrhalis* are rare, but are observed in immunocompromised individuals (Aebi, C., et al, 1998. Infect. Immun. 66:540-548.). Concern for *M. catarrhalis* infections of cystic fibrosis (CF) patients is growing. Damage to the respiratory tract by *M. catarrhalis* could promote invasion by other pathogens such as *P. aeruginosa* in CF patients. (Deneuve, E., et al, 1995. ACTA Paediatr. 84:1212.). *M. catarrhalis* is also associated with acute laryngitis. In one study, 50% of patients with acute laryngitis were colonized with *M. catarrhalis* (Hol, C., et al, 1996. Journal of Infectious Diseases. 174:636-638.), while isolates from healthy adults occur at the rate of 6% -11%. The colonization rates of children can be much higher, with average rates of 30%-35% (Sehgal, SC. et al, 1994. Infection 22:193-196.). In some hospitals, *M. catarrhalis* accounts for half of all the respiratory infections (Bluesone, C., et al, 1992. Pediatr. Infect. Dis. J. 11:S7-S11.).

Increasing levels of antibiotic resistance have been observed in clinical isolates of *M. catarrhalis* recently. Before 1980, less than 10% of *M. catarrhalis* isolates were β -lactamase-positive. Currently, most clinical isolates produce β -lactamase, making them resistant to β -lactam antibiotics such as penicillin. (Doern, G., et al, 1996. Antimicrob.

Agents Chemother. 40:2884-2886.). *M. catarrhalis* is intrinsically resistant to a small group of drugs that include vancomycin and trimethoprim (Wallace, RJ. 1990. Am. J. Med. 88:46S-50S), and is becoming increasingly resistant to sulfamethoxazole, oral cephalosporins, and macrolides (Hoppe, HL. 1998. Am. J. Health. Syst. Pharm. 55:1881-97).

5 Although, *M. catarrhalis* was once considered only as part of the nonpathogenic flora of the upper respiratory tract, it is emerging as an important respiratory pathogen. Currently, it is the third leading cause of lower respiratory tract infections and otitis media. Sequencing and further analysis of this genome will aid in identification of essential genes for development of drug targets, and reduce the health threat this organism poses.

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SUMMARY OF THE INVENTION

The present invention fulfills the need for diagnostic tools and therapeutics by providing bacterial-specific compositions and methods for detecting *Moraxella* species including *M. catarrhalis*, as well as compositions and methods useful for treating and
15 preventing *Moraxella* infection, in particular, *M. catarrhalis* infection, in vertebrates including mammals.

The present invention encompasses isolated nucleic acids and polypeptides derived from *M. catarrhalis* that are useful as reagents for diagnosis of bacterial disease, components of effective antibacterial vaccines, and/or as targets for antibacterial drugs including anti-*M.*
20 *catarrhalis* drugs. They can also be used to detect the presence of *M. catarrhalis* and other *Moraxella* species in a sample; and in screening compounds for the ability to interfere with the *M. catarrhalis* life cycle or to inhibit *M. catarrhalis* infection. They also have use as biocontrol agents for plants.

In one aspect, the invention features compositions of nucleic acids corresponding to
25 entire coding sequences of *M. catarrhalis* proteins (SEQ ID NO: 1 - SEQ ID NO: 1920), including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *M. catarrhalis* proteins to block protein translation, and methods for producing *M. catarrhalis* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to

detect *M. catarrhalis* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *M. catarrhalis* are within the scope of this invention.

The nucleotide sequences provided in SEQ ID NO: 1 - SEQ ID NO: 1920, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 1920 may be "provided" in a variety of medias to facilitate use thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NO: 1 - SEQ ID NO: 1920, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 1920. Uses for and methods for providing nucleotide sequences in a variety of media is well known in the art (see e.g., EPO Publication No. EP 0 756 006).

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage media, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A person skilled in the art can readily appreciate how any of the presently known computer readable media can be used to create a manufacture comprising computer readable media having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable media. A person skilled in the art can readily adopt any of the presently known methods for recording information on computer readable media to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a person skilled in the art for creating a computer readable media having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the

present invention on computer readable media. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A person skilled in the art can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable media having recorded thereon the nucleotide sequence information of the present invention.

By providing the nucleotide sequence of SEQ ID NO: 1 - SEQ ID NO: 1920, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to SEQ ID NO: 1 - SEQ ID NO: 1920 in computer readable form, a person skilled in the art can routinely access the coding sequence information for a variety of purposes. Computer software is publicly available which allows a person skilled in the art to access sequence information provided in a computer readable media. Examples of such computer software include programs of the "Staden Package", "DNA Star", "MacVector", GCG "Wisconsin Package" (Genetics Computer Group, Madison, WI) and "NCBI Toolbox" (National Center For Biotechnology Information). Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Computer algorithms enable the identification of *M. catarrhalis* open reading frames (ORFs) within SEQ ID NO: 1 - SEQ ID NO: 1920 which contain homology to ORFs or proteins from other organisms. Examples of such similarity-search algorithms include the BLAST [Altschul et al., J. Mol. Biol. 215:403-410 (1990)] and Smith-Waterman [Smith and Waterman (1981) *Advances in Applied Mathematics*, 2:482-489] search algorithms. Suitable search algorithms are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). Such algorithms are utilized on computer systems as exemplified

below. The ORFs so identified represent protein encoding fragments within the *M. catarrhalis* genome and *M. catarrhalis* plasmids and are useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

5 The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *M. catarrhalis* genome and plasmids. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present
10 invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A person skilled in the art can readily appreciate that any one of the currently available computer-based systems is suitable for use in the present invention. The computer-based systems of the present invention comprise a data storage means having stored therein a
15 nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

20 As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *M. catarrhalis* genome and plasmids which are similar to, or "match", a particular target sequence or target motif. A variety of known
25 algorithms are known in the art and have been disclosed publicly, and a variety of commercially available software for conducting homology-based similarity searches are available and can be used in the computer-based systems of the present invention. Examples of such software includes, but is not limited to, FASTA (GCG Wisconsin Package), Bic_SW (Compugen Bioccelerator), BLASTN2, BLASTP2, BLASTX2 (NCBI) and Motifs (GCG).
30 Suitable software programs are described, for example, in Martin J. Bishop, ed., *Guide to*

Human Genome Computing, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). A person skilled in the art can readily recognize that any one of
5 the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A person skilled in the art can readily recognize that the longer a target sequence is, the less likely a target sequence will be present
10 as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that many genes are longer than 500 amino acids, or 1.5 kb in length, and that commercially important fragments of the *M. catarrhalis* genome and plasmids from *M. catarrhalis*, such as sequence fragments involved in gene expression and
15 protein processing, will often be shorter than 30 nucleotides.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a specific functional domain or three-dimensional configuration which is formed upon the folding of the target polypeptide. There are a variety of target motifs known in the art.
20 Protein target motifs include, but are not limited to, enzymatic active sites, membrane-spanning regions, and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input
25 and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *M. catarrhalis* genome and plasmids possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a person skilled in the art with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of
30 homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *M. catarrhalis* genome and plasmids. In the present examples, implementing software which implement the BLASTP2 and bic_SW algorithms (Altschul et al., J Mol. Biol. 215:403-410 (1990);
5 Compugen Biocellator) was used to identify open reading frames within the *M. catarrhalis* genome and plasmids. A person skilled in the art can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition,
10 Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

The invention features *M. catarrhalis* polypeptides, preferably a substantially pure preparation of an *M. catarrhalis* polypeptide, or a recombinant *M. catarrhalis* polypeptide.
15 In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with
20 an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acid residues in length; the polypeptide includes at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least about 50, 100, or
25 150 contiguous amino acid residues of the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *M. catarrhalis* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

In preferred embodiments: the *M. catarrhalis* polypeptide is encoded by a nucleic
30 acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least

about 60%, 70%, 80%, 90%, 95%, 98%, or 99% sequence identity or % homology with a nucleic acid of the invention contained in the Sequence Listing.

5 In a preferred embodiment, the subject *M. catarrhalis* polypeptide differs in amino acid sequence at about 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *M. catarrhalis* polypeptide exhibits an *M. catarrhalis* biological activity, e.g., the *M. catarrhalis* polypeptide retains a biological activity of a naturally occurring *M. catarrhalis* enzyme.

10 In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

15 In yet other preferred embodiments, the *M. catarrhalis* polypeptide is a recombinant fusion protein having a first *M. catarrhalis* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *M. catarrhalis*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

20 Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

25 In a preferred embodiment, the encoded *M. catarrhalis* polypeptide differs (e.g., by amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at about 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *M. catarrhalis* encoded polypeptide exhibits an *M. catarrhalis* biological activity, e.g., the encoded *M. catarrhalis* enzyme retains a biological activity of a naturally occurring *M. catarrhalis*.

30 In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading

frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

5 The *M. catarrhalis* strain, 98-4362, from which genomic sequences have been sequenced, has been deposited on July 20, 1998, in the American Type Culture Collection and assigned the ATCC designation # 202156.

10 Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridize under high or low stringency conditions to a nucleic acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *M. catarrhalis* polypeptides, especially by antisera to an active site or binding domain of *M. catarrhalis* polypeptide. The invention also includes fragments, preferably biologically active fragments. These and other
15 polypeptides are also referred to herein as *M. catarrhalis* polypeptide analogs or variants.

The invention further provides nucleic acids, e.g., RNA or DNA and their respective complements, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

20 In preferred embodiments, the subject *M. catarrhalis* nucleic acid will include a transcriptional regulatory sequence, e.g., at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *M. catarrhalis* gene sequence, e.g., to render the *M. catarrhalis* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *M. catarrhalis* polypeptide of the invention, hybridizes under stringent conditions to a nucleic
25 acid probe corresponding to at least about 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 12 consecutive nucleotides of the invention contained in the Sequence Listing; still more preferably to at least about 20 consecutive nucleotides of the invention contained in the Sequence Listing; most preferably to at least about 40 consecutive nucleotides of the invention contained in the
30 Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *M. catarrhalis* polypeptide. In preferred embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98% or 99% homologous to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least about 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *M. catarrhalis* polypeptide or an *M. catarrhalis* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *M. catarrhalis* polypeptide or *M. catarrhalis* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating an *M. catarrhalis* or *M. catarrhalis* polypeptide variant, e.g., from the cell or from the cell culture medium.

One embodiment of the invention is directed to substantially isolated nucleic acids. Nucleic acids of the invention include sequences comprising at least about 8 nucleotides in length, more preferably at least about 12 nucleotides in length, even more preferably at least about 15-20 nucleotides in length, that correspond to a subsequence of any one of SEQ ID NO: 1 - SEQ ID NO: 1920 or complements thereof. Alternatively, the nucleic acids comprise sequences contained within any ORF (open reading frame), including a complete protein-coding sequence, of which any of SEQ ID NO: 1 - SEQ ID NO: 1920 forms a part. The invention encompasses sequence-conservative variants and function-conservative variants of these sequences. The nucleic acids may be DNA, RNA, DNA/RNA duplexes, protein-nucleic acid (PNA), or derivatives thereof.

In another aspect, the invention features a purified recombinant nucleic acid having at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence of the invention contained in the Sequence Listing

The invention also encompasses recombinant DNA (including DNA cloning and expression vectors) comprising these *M. catarrhalis* -derived sequences; host cells comprising such DNA, including fungal, bacterial, yeast, plant, insect, and mammalian host cells; and methods for producing expression products comprising RNA and polypeptides encoded by the *M. catarrhalis* sequences. These methods are carried out by incubating a host cell comprising an *M. catarrhalis* -derived nucleic acid sequence under conditions in which the sequence is expressed. The host cell may be native or recombinant. The polypeptides can be obtained by (a) harvesting the incubated cells to produce a cell fraction and a medium fraction; and (b) recovering the *M. catarrhalis* polypeptide from the cell fraction, the medium fraction, or both. The polypeptides can also be made by *in vitro* translation.

In another aspect, the invention features nucleic acids capable of binding mRNA of *M. catarrhalis*. Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *M. catarrhalis*. A further aspect features a nucleic acid which is capable of binding specifically to an *M. catarrhalis* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *M. catarrhalis* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *M. catarrhalis* nucleic acid.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *M. catarrhalis* polypeptide or an *M. catarrhalis* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *M. catarrhalis* polypeptide or *M. catarrhalis* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *M. catarrhalis* or *M. catarrhalis* polypeptide variant, e.g., from the cell or from the cell culture medium.

In yet another embodiment of the invention encompasses reagents for detecting bacterial infection, including *M. catarrhalis* infection, which comprise at least one *M. catarrhalis* -derived nucleic acid defined by any one of SEQ ID NO: 1 - SEQ ID NO: 1920, or sequence-conservative or function-conservative variants thereof. Alternatively, the

diagnostic reagents comprise nucleotide sequences that are contained within any open reading frames (ORFs), including preferably complete protein-coding sequences, contained within any of SEQ ID NO: 1 - SEQ ID NO: 1920, or polypeptide sequences contained within any of SEQ ID NO: 1921 - SEQ ID NO: 3840, or polypeptides of which any of the above
5 sequences forms a part, or antibodies directed against any of the above peptide sequences or function-conservative variants and/or fragments thereof.

The invention further provides antibodies, preferably monoclonal antibodies, which specifically bind to the polypeptides of the invention. Methods are also provided for producing antibodies in a host animal. The methods of the invention comprise immunizing
10 an animal with at least one *M. catarrhalis* -derived immunogenic component, wherein the immunogenic component comprises one or more of the polypeptides encoded by any one of SEQ ID NO: 1 - SEQ ID NO: 1920 or sequence-conservative or function-conservative variants thereof; or polypeptides that are contained within any ORFs, including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 1920 forms a part;
15 or polypeptide sequences contained within any of SEQ ID NO: 1921 - SEQ ID NO: 3840; or polypeptides of which any of SEQ ID NO: 1921 - SEQ ID NO: 3840 forms a part. Host animals include any warm blooded animal, including without limitation mammals and birds. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *M. catarrhalis* -specific antigens.

20 In yet another aspect, the invention provides diagnostic methods for detecting *M. catarrhalis* antigenic components or anti-*M. catarrhalis* antibodies in a sample. *M. catarrhalis* antigenic components may be detected by known processes, including but not limited to detection by a process comprising: (i) contacting a sample suspected to contain a bacterial antigenic component with a bacterial-specific antibody, under conditions in which a
25 stable antigen-antibody complex can form between the antibody and bacterial antigenic components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of at least one bacterial antigenic component in the sample. In different embodiments of this method, the antibodies used are directed against a sequence encoded by any of SEQ ID NO: 1 - SEQ ID
30 NO: 1920 or sequence-conservative or function-conservative variants thereof, or against a

polypeptide sequence contained in any of SEQ ID NO: 1921 - SEQ ID NO: 3840 or function-conservative variants thereof.

In yet another aspect, the invention provides a method for detecting antibacterial-specific antibodies in a sample, which comprises: (i) contacting a sample suspected to contain antibacterial-specific antibodies with an *M. catarrhalis* antigenic component, under conditions in which a stable antigen-antibody complex can form between the *M. catarrhalis* antigenic component and antibacterial antibodies in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of antibacterial antibodies in the sample. In different embodiments of this method, the antigenic component is encoded by a sequence contained in any of SEQ ID NO: 1 - SEQ ID NO: 1920 or sequence-conservative and function-conservative variants thereof, or is a polypeptide sequence contained in any of SEQ ID NO: 1921 - SEQ ID NO: 3840 or function-conservative variants thereof.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *M. catarrhalis*. The method includes: immunizing a subject with an *M. catarrhalis* polypeptide, e.g., a surface or secreted polypeptide, or a combination of such peptides or active portion(s) thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *M. catarrhalis* polypeptide. The method includes contacting the compound to be evaluated with an *M. catarrhalis* polypeptide and determining if the compound binds or otherwise interacts with the *M. catarrhalis* polypeptide. Compounds which bind or otherwise interact with *M. catarrhalis* polypeptides are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *M. catarrhalis* nucleic acid, e.g., DNA or RNA. The method includes contacting the compound to be evaluated with an *M. catarrhalis* nucleic acid and determining if the compound binds or otherwise interacts with the *M. catarrhalis* nucleic acid. Compounds which bind *M.*

catarrhalis are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

A particularly preferred embodiment of the invention is directed to a method of screening test compounds for anti-bacterial activity, which method comprises: selecting as a target a bacterial specific sequence, which sequence is essential to the viability of a bacterial species; contacting a test compound with said target sequence; and selecting those test compounds which bind to said target sequence as potential anti-bacterial candidates. In one embodiment, the target sequence selected is specific to a single species, or even a single strain, such as, for example, the strain *M. catarrhalis* 98-4362. In a second embodiment, the target sequence is common to at least two species of bacteria. In a third embodiment, the target sequence is common to a family of bacteria. The target sequence may be a nucleic acid sequence or a polypeptide sequence. Methods employing sequences common to more than one species of microorganism may be used to screen candidates for broad spectrum anti-bacterial activity.

The invention also provides methods for preventing or treating disease caused by certain bacteria, including *M. catarrhalis*, which are carried out by administering to an animal in need of such treatment, in particular a warm-blooded vertebrate, including but not limited to birds and mammals, a compound that specifically inhibits or interferes with the function of a bacterial polypeptide or nucleic acid. In a particularly preferred embodiment, the mammal to be treated is human.

DETAILED DESCRIPTION OF THE INVENTION

The sequences of the present invention include the specific nucleic acid and amino acid sequences set forth in the Sequence Listing that forms a part of the present specification, and which are designated SEQ ID NO: 1 - SEQ ID NO: 3840. Use of the terms "SEQ ID NO: 1 - SEQ ID NO: 1920", "SEQ ID NO: 1921 - SEQ ID NO: 3840", "the sequences depicted in Table 2", etc., is intended, for convenience, to refer to each individual SEQ ID NO *individually*, and is not intended to refer to the genus of these sequences unless such reference would be indicated. In other words, it is a shorthand for listing all of these

sequences individually. The invention encompasses each sequence individually, as well as any combination thereof.

DEFINITIONS

5 "Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, i.e., DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes
10 nucleic acids containing modified bases.

A nucleic acid or polypeptide sequence that is "derived from" a designated sequence refers to a sequence that corresponds to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants."
15 For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative variants are those in which a change of one or more nucleotides in a given codon position results in no alteration in the amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native
20 polypeptide, including, but not limited to, replacement of an amino acid with one having similar physico-chemical properties (such as, for example, acidic, basic, hydrophobic, and the like). "Function-conservative" variants also include any polypeptides that have the ability to elicit antibodies specific to a designated polypeptide.

An "*M. catarrhalis* -derived" nucleic acid or polypeptide sequence may or may not be
25 present in other bacterial species, and may or may not be present in all *M. catarrhalis* strains. This term is intended to refer to the source from which the sequence was originally isolated. Thus, an *M. catarrhalis* -derived polypeptide, as used herein, may be used, e.g., as a target to screen for a broad spectrum antibacterial agent, to search for homologous proteins in other species of bacteria or in eukaryotic organisms such as bacteria humans, etc.

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs. Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least about 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains sufficient polypeptide to allow protein sequencing; at least about 1, 10, or preferably 100 mg of polypeptide.

A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least about 10%, more preferably at least about 50%, of the subject cells.

A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome and plasmids of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *M. catarrhalis* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA,
5 synthetic DNA, and recombinant nucleic acid sequences.

A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a
10 gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties,
15 fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of
20 hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

"Homologous" refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a
25 position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two
30 sequences are matched or homologous then the two sequences are 60% homologous. By

way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid
5 can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated.
10 Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C) require correspondingly less overall complementarity between the hybridizing sequences. (1X SSC is 0.15 M NaCl,
15 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

20 A polypeptide has *M. catarrhalis* biological activity if it has one, two or preferably more of the following properties: (1) if when expressed in the course of an *M. catarrhalis* infection, it can promote, or mediate the attachment of *M. catarrhalis* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *M. catarrhalis* protein; (3) the gene which encodes it can rescue a lethal mutation in an *M. catarrhalis* gene.
25 A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *M. catarrhalis* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *M. catarrhalis* polypeptides, e.g., one or
30 more of the biological activities described herein. Especially preferred are fragments which

exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO (Chinese Hamster Ovary) cells. Because peptides such as *M. catarrhalis* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *M. catarrhalis* fragment or *M. catarrhalis* analog is one which exhibits a biological activity in any biological assay for *M. catarrhalis* activity. The fragment or analog possesses about 10%, preferably about 40%, more preferably about 60%, 70%, 80% or 90% or greater of the activity of *M. catarrhalis*, in any *in vivo* or *in vitro* assay.

Analogues can differ from naturally occurring *M. catarrhalis* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogues include *M. catarrhalis* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *M. catarrhalis* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

TABLE 1

CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys

Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	D	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid
Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-
5 naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *M. catarrhalis* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *M. catarrhalis* polypeptides can be generated by methods known to those skilled in the art. The ability of an *Moraxella*
10 fragment to exhibit a biological activity of *M. catarrhalis* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *M. catarrhalis* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

15 An "immunogenic component" as used herein is a moiety, such as an *M. catarrhalis* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *M. catarrhalis* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with
20 sufficiently high affinity to form a detectable antigen-antibody complex.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *M. catarrhalis* polypeptides.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the
25 promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of
30 expression that differs from wild type in terms of the time or stage at which the gene is

expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of increased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

10 As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original parent, due to accident or deliberate mutation.

As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved under conditions compatible with the control sequence and host cell.

The "metabolism" of a substance, as used herein, means any aspect of the expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present invention pertains, unless otherwise defined. Reference is made herein to various methodologies known to those of skill in the art. Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full. The practice of the invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, *Molecular Cloning; Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.); *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991); *Immunology*, 2d Edition, 1989, Roitt *et al.*, C.V. Mosby Company, and New York; *Advanced Immunology*, 2d Edition, 1991, Male *et al.*, Grower Medical Publishing, New York.; *DNA Cloning: A Practical Approach*, Volumes I and II, 1985 (D.N. Glover ed.); *Oligonucleotide Synthesis*, 1984, (M.L. Gait ed); *Transcription and Translation*, 1984 (Hames and Higgins eds.); *Animal Cell Culture*, 1986 (R.I. Freshney ed.); *Immobilized Cells and Enzymes*, 1986 (IRL Press); Perbal, 1984, A

- Practical Guide to Molecular Cloning; Gene Transfer Vectors for Mammalian Cells*, 1987 (J. H. Miller and M. P. Calos eds., Cold Spring Harbor Laboratory); Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Any suitable materials and/or methods known to those of skill can be utilized in carrying out the present invention; however, preferred materials and/or methods are described. Materials, reagents and the like to which reference is made in the following description and examples are obtainable from commercial sources, unless otherwise noted.

M. CATARRHALIS GENOMIC SEQUENCE

This invention provides nucleotide sequences of the genome of *M. catarrhalis* which thus comprises a DNA sequence library of *M. catarrhalis* genomic DNA. The detailed description that follows provides nucleotide sequences of *M. catarrhalis*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are compositions and methods of using the disclosed *M. catarrhalis* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *M. catarrhalis*.

To determine the genomic sequence of *M. catarrhalis*, DNA from strain 98-4362. of *M. catarrhalis* was isolated and a library of DNA fragments were transformed into DH5a cells. DNA sequencing was achieved using established ABI sequencing methods on ABI377 automated DNA sequencers. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The cloning and sequencing procedures are described in more detail in the Exemplification.

5 A variety of approaches may be used to order the contigs so as to obtain a continuous sequence representing the entire *M. catarrhalis* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libraries of *M. catarrhalis* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then
10 used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.

The *M. catarrhalis* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on
15 stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *M. catarrhalis* polypeptide. These ORFs may contain start codons which indicate the initiation of protein synthesis of a naturally-occurring *M. catarrhalis* polypeptide. Such start codons within the ORFs provided herein were identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *M.*
20 *catarrhalis* polypeptide is within the scope of this invention. For example, within the ORFs a codon such as AUG or GUG (encoding methionine or valine) which is part of the initiation signal for protein synthesis were identified and the portion of an ORF to corresponding to a naturally-occurring *M. catarrhalis* polypeptide was recognized. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program
25 GENEMARK™ (Borodovsky and McIninch, 1993, *Comp. . 17*:123).

Each predicted ORF amino acid sequence was compared with all sequences found in current GENBANK, SWISS-PROT, and PIR databases using the BLAST algorithm. BLAST identifies local alignments occurring by chance between the ORF sequence and the sequence in the databank (Altschall et al., 1990, *L Mol. Biol.* 215:403-410). Homologous ORFs
30 (probabilities less than 10^{-5} by chance) and ORF's that are probably non-homologous

(probabilities greater than 10^{-5} by chance) but have good codon usage were identified. Both homologous, sequences and non-homologous sequences with good codon usage, are likely to encode proteins and are encompassed by the invention.

5 *M. CATARRHALIS* NUCLEIC ACIDS

The present invention provides a library of *M. catarrhalis* -derived nucleic acid sequences. The libraries provide probes, primers, and markers which are used as markers in epidemiological studies. The present invention also provides a library of *M. catarrhalis* -derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

10 The nucleic acids of this invention may be obtained directly from the DNA of the above referenced *M. catarrhalis* strain by using the polymerase chain reaction (PCR). See "*PCR, A Practical Approach*" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK, 1991) for details about the PCR. High fidelity PCR is used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products is verified by
15 conventional sequencing methods. Clones carrying the desired sequences described in this invention may also be obtained by screening the libraries by means of the PCR or by hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

20 It is also possible to obtain nucleic acids encoding *M. catarrhalis* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *M. catarrhalis* polypeptide can be obtained by isolating total mRNA from an appropriate strain. Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any
25 one of a number of known techniques. Genes encoding *M. catarrhalis* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See e.g., Itakura et al. U.S. Patent No. 4,598,049; 5 Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

In another example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 264:17078, or other well known 10 methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Nucleic acids isolated or synthesized in accordance with features of the present invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins 15 and peptides corresponding to such sequences. As probes, primers, capture ligands and antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products) of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

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PROBES

A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *M. catarrhalis*. With the sequence information set forth in the present application, sequences 25 of twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *M. catarrhalis*, and extraneous nucleic acids likely to be encountered during hybridization conditions. More preferably, the sequence will comprise at least about twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

- 5 Nucleic acid isolated and synthesized in accordance with the sequence of the invention contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Moraxella* species using appropriate stringency hybridization conditions as described herein.

10 CAPTURE LIGAND

- For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing have utility to
- 15 separate *M. catarrhalis* nucleic acid from one strain from the nucleic acid of other another strain as well as from other organisms. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate other *Moraxella* species from each other and from other organisms. Preferably, the sequence will comprise at least about twenty nucleotides to convey stability to the hybridization
- 20 product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

PRIMERS

- 25 Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility as primers for the amplification of *M. catarrhalis* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other *Moraxella* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of ≥ 10 -15 nucleotides of the invention contained in the Sequence Listing
- 30 have utility in conjunction with suitable enzymes and reagents to create copies of *M.*

catarrhalis nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including genes from *M. catarrhalis* and/or other *Moraxella* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail herein.

The nucleic acids of the present invention find use as templates for the recombinant production of *M. catarrhalis* -derived peptides or polypeptides

ANTISENSE

Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *M. catarrhalis* genes. These sequences also have utility as antisense agents to prevent expression of genes of other *Moraxella* species.

In one embodiment, nucleic acid or derivatives corresponding to *M. catarrhalis* nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

The present invention encompasses isolated polypeptides and nucleic acids derived from *M. catarrhalis* that are useful as reagents for diagnosis of bacterial infection, components of effective anti-bacterial vaccines, and/or as targets for anti-bacterial drugs, including anti-*M. catarrhalis* drugs.

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EXPRESSION OF *M. CATARRHALIS* NUCLEIC ACIDS

Table 2, which is appended herewith and which forms part of the present specification, provides a list of open reading frames (ORFs) in both strands and a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLASTP2 algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. An ORF is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and was determined from stop to stop codons. The first column contains a designation for the ORF ("ORF Name"). The second and third columns list the SEQ ID numbers for the nucleic acid ("NT ID") and amino acid ("AA ID") sequences corresponding to each ORF, respectively. The fourth and fifth columns list the length of the nucleic acid ORF ("NT Length") and the length of the amino acid ORF ("AA Length"), respectively. The nucleotide sequence corresponding to each ORF begins at the first nucleotide immediately following a stop codon and ends at the nucleotide immediately preceding the next downstream stop codon in the same reading frame. It will be recognized by one skilled in the art that the natural translation initiation sites will correspond to ATG, GTG, or TTG codons located within the ORFs. The natural initiation sites depend not only on the sequence of a start codon but also on the context of the DNA sequence adjacent to the start codon. Usually, a recognizable ribosome binding site is found within 20 nucleotides upstream from the initiation codon. In some cases where genes are translationally coupled and coordinately expressed together in "operons", ribosome binding sites are not present, but the initiation codon of a downstream gene may occur very close to, or overlap, the stop codon of the an upstream gene in the same operon. The correct start codons can be generally identified without undue experimentation because only a few codons need be tested. It is recognized that the translational machinery in bacteria initiates all polypeptide chains with

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the amino acid methionine, regardless of the sequence of the start codon. In some cases, polypeptides are post-translationally modified, resulting in an N-terminal amino acid other than methionine *in vivo*. The sixth and seventh columns provide metrics for assessing the likelihood of the homology match (determined by the BLASTP2 algorithm), as is known in the art, to the genes indicated in the description frame ("Description") defined further below. These genes in the Description were identified when the designated ORF was compared against a comprehensive non-redundant protein database. Specifically, the sixth column represents the Blast Score ("Score") for the match (a higher score is a better match), and the seventh column represents the probability ("Probability") for the match (the probability that such a match can have occurred by chance; the lower the value, the more likely the match is valid). If a BLASTP2 score of less than 100 was obtained, no value is reported in the table. The remaining fields below the columns contain additional information relating to the potential function of the sequence based on the BLASTP2 analysis. Where a match was discovered, the field "Protein name" list the protein's name identified from the match. In addition, one skilled in the art would be able to identify the match and elucidate its function using the "Locus name" and where available the accession number, "Acc#" from the database. Lastly, one skilled in the art would appreciate the "Description" field to further describe the potential function of the protein based on this analysis. This information allows one of ordinary skill in the art to determine a potential use for each identified coding sequence and, as a result, allows to use the polypeptides of the present invention for commercial and industrial purposes.

Using the information provided in SEQ ID NO: 1 - SEQ ID NO: 1920, SEQ ID NO: 1921 - SEQ ID NO: 3840 and in Table 2 together with routine cloning and sequencing methods, one of ordinary skill in the art will be able to clone and sequence all the nucleic acid fragments of interest including open reading frames (ORFs) encoding a large variety of proteins of *M. catarrhalis*.

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in SEQ ID NO: 1 - SEQ ID NO: 1920 and in Table 2 or fragments of said nucleic acid encoding active portions of *M. catarrhalis* polypeptides can be cloned into suitable vectors

or used to isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

5 The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the same gene product(s). This includes, but is not limited to, Eucaryotic species such as the yeast
10 *Saccharomyces cerevisiae*, *Methanobacterium* strains or other Archaea, and Eubacteria such as *E. coli*, *B. Subtilis*, *S. Aureus*, *S. Pneumonia* or *Pseudomonas putida*. In some cases the expression host will utilize the natural *M. catarrhalis* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

15 To express a gene product using the natural *M. catarrhalis* promoter, a procedure such as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable
20 marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and cells containing the recombinant plasmid are identified by
25 selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR

amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell. Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press (1989)),
5 and other laboratory textbooks.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *M. catarrhalis* polypeptide can be cultured under appropriate conditions to allow expression of the polypeptide to occur. Suitable media for
10 cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such polypeptides. Additionally, in many situations, polypeptides can be produced by chemical
15 cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized complex, where the membrane-associated protein is no longer entirely embedded in the
20 membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Chromatographic techniques which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *M. catarrhalis* peptide expression in *E. coli* is
25 to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding an *M. catarrhalis* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those
30 preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids*

Res. 20:2111-2118). Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

5 The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

10 The present invention provides a library of *M. catarrhalis* -derived nucleic acid sequences. The libraries provide probes, primers, and markers which can be used as markers in epidemiological studies. The present invention also provides a library of *M. catarrhalis* -derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

15 Nucleic acids comprising any of the sequences disclosed herein or sub-sequences thereof can be prepared by standard methods using the nucleic acid sequence information provided in SEQ ID NO: 1 - SEQ ID NO: 1920. For example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 764:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

20 Of course, due to the degeneracy of the genetic code, many different nucleotide sequences can encode polypeptides having the amino acid sequences defined by SEQ ID NO: 1921 - SEQ ID NO: 3840 or sub-sequences thereof. The codons can be selected for optimal expression in prokaryotic or eukaryotic systems. Such degenerate variants are also encompassed by this invention.

25 Insertion of nucleic acids (typically DNAs) encoding the polypeptides of the invention into a vector is easily accomplished when the termini of both the DNAs and the vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to

achieve the same result by filling in the single-stranded termini with an appropriate DNA polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki *et al.*, 1988, *Science* 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

The nucleic acids of the invention may be isolated directly from cells. Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or genomic material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

The nucleic acids of the present invention may be flanked by natural *M. catarrhalis* regulatory sequences, or may be associated with heterologous sequences, including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and 3'- noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also included. The nucleic acid may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the nucleic acid sequences of the present invention may also be modified with

a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

5 The invention also provides nucleic acid vectors comprising the disclosed *M. catarrhalis* -derived sequences or derivatives or fragments thereof. A large number of vectors, including plasmid and bacterial vectors, have been described for replication and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for cloning or protein expression.

10 The encoded *M. catarrhalis* polypeptides may be expressed by using many known vectors, such as pUC plasmids, pET plasmids (Novagen, Inc., Madison, WI), or pRSET or pREP (Invitrogen, San Diego, CA), and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

15 Recombinant cloning vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, e.g. antibiotic resistance, and one or more expression cassettes. The inserted *M. catarrhalis* coding sequences may be synthesized by standard methods, isolated from natural sources, or prepared as hybrids, etc. Ligation of the *M. catarrhalis* coding sequences to transcriptional regulatory elements and/or to other amino acid coding sequences may be achieved by known methods. Suitable host cells may be transformed/transfected/infected as appropriate by any
20 suitable method including electroporation, CaCl₂ mediated DNA uptake, bacterial infection, microinjection, microprojectile, or other established methods.

Appropriate host cells include bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *M. catarrhalis*, *E. coli*, *B. Subtilis*, *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*,
25 *Schizosaccharomyces pombe*, SF9 cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of
30 heterologous proteins in the various hosts. Examples of these regions, methods of isolation,

manner of manipulation, etc. are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced *M. catarrhalis* -derived peptides and polypeptides.

Advantageously, vectors may also include a transcription regulatory element (i.e., a promoter) operably linked to the *M. catarrhalis* portion. The promoter may optionally contain operator portions and/or ribosome binding sites. Non-limiting examples of bacterial promoters compatible with *E. coli* include: b-lactamase (penicillinase) promoter; lactose promoter; tryptophan (trp) promoter; araBAD (arabinose) operon promoter; lambda-derived P₁ promoter and N gene ribosome binding site; and the hybrid tac promoter derived from sequences of the trp and lac UV5 promoters. Non-limiting examples of yeast promoters include 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactoeprimase promoter, and alcohol dehydrogenase (ADH) promoter. Suitable promoters for mammalian cells include without limitation viral promoters such as that from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences, polyA addition sequences and enhancer sequences to increase expression. Sequences which cause amplification of the gene may also be desirable. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or prohormone pro region sequences, may also be included. These sequences are well described in the art.

Nucleic acids encoding wild-type or variant *M. catarrhalis* -derived polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene. Other recombination-based methods such as nonhomologous recombinations or deletion of endogenous genes by homologous recombination may also be used.

The nucleic acids of the present invention find use as templates for the recombinant production of *M. catarrhalis* -derived peptides or polypeptides.

IDENTIFICATION AND USE OF *M. CATARRHALIS* NUCLEIC ACID SEQUENCES

The disclosed *M. catarrhalis* polypeptide and nucleic acid sequences, or other sequences that are contained within ORFs, including complete protein-coding sequences, of which any of the disclosed *M. catarrhalis* -specific sequences forms a part, are useful as
5 target components for diagnosis and/or treatment of *M. catarrhalis* - caused infection

It will be understood that the sequence of an entire protein-coding sequence of which each disclosed nucleic acid sequence forms a part can be isolated and identified based on each disclosed sequence. This can be achieved, for example, by using an isolated nucleic acid encoding the disclosed sequence, or fragments thereof, to prime a sequencing reaction
10 with genomic *M. catarrhalis* DNA as template; this is followed by sequencing the amplified product. The isolated nucleic acid encoding the disclosed sequence, or fragments thereof, can also be hybridized to *M. catarrhalis* genomic libraries to identify clones containing additional complete segments of the protein-coding sequence of which the shorter sequence forms a part. Then, the entire protein-coding sequence, or fragments thereof, or nucleic
15 acids encoding all or part of the sequence, or sequence-conservative or function-conservative variants thereof, may be employed in practicing the present invention.

Preferred sequences are those that are useful in diagnostic and/or therapeutic applications. Diagnostic applications include without limitation nucleic-acid-based and antibody-based methods for detecting bacterial infection. Therapeutic applications include
20 without limitation vaccines, passive immunotherapy, and drug treatments directed against gene products that are both unique to bacteria and essential for growth and/or replication of bacteria.

IDENTIFICATION OF NUCLEIC ACIDS ENCODING VACCINE COMPONENTS AND 25 TARGETS FOR AGENTS EFFECTIVE AGAINST *M. CATARRHALIS*

The disclosed *M. catarrhalis* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for
30 agents effective against *M. catarrhalis*. Identification of said immunogenic components

involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

5 HOMOLOGY TO KNOWN SEQUENCES:

Computer-assisted comparison of the disclosed *M. catarrhalis* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *M. catarrhalis* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *M. catarrhalis* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antibacterial drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal peptides and hydrophobic transmembrane domains. *M. catarrhalis* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

Targets for therapeutic drugs according to the invention include, but are not limited to, polypeptides of the invention, whether unique to *M. catarrhalis* or not, that are essential for growth and/or viability of *M. catarrhalis* under at least one growth condition. Polypeptides essential for growth and/or viability can be determined by examining the effect

of deleting and/or disrupting the genes, i.e., by so-called gene "knockout". Alternatively, genetic fingerprinting can be used (Smith *et al.*, 1995, *Proc. Natl. Acad. Sci. USA* 92:5479-6433; Published International Application WO 94/26933; U.S. Patent No. 5,612,180). Still other methods for assessing essentiality includes the ability to isolate conditional lethal
5 mutations in the specific gene (e.g., temperature sensitive mutations). Other useful targets for therapeutic drugs, which include polypeptides that are not essential for growth or viability *per se* but lead to loss of viability of the cell, can be used to target therapeutic agents to cells.

10 STRAIN-SPECIFIC SEQUENCES:

Because of the evolutionary relationship between different *M. catarrhalis* strains, it is believed that the presently disclosed *M. catarrhalis* sequences are useful for identifying, and/or discriminating between, previously known and new *M. catarrhalis* strains. It is believed that other *M. catarrhalis* strains will exhibit at least about 70% sequence homology
15 with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *M. catarrhalis* strains, and comparison with the present sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *M. catarrhalis* strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide
20 sequences that discriminate between different strains of *M. catarrhalis*. Strain-specific components can also be identified functionally by their ability to elicit or react with antibodies that selectively recognize one or more *M. catarrhalis* strains.

In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *M. catarrhalis* strains but are not
25 found in other bacterial species.

M. CATARRHALIS POLYPEPTIDES

This invention encompasses isolated *M. catarrhalis* polypeptides encoded by the disclosed *M. catarrhalis* genomic sequences, including the polypeptides of the invention
30 contained in the Sequence Listing. Polypeptides of the invention are preferably at least

about 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding an *M. catarrhalis* polypeptide can be isolated and identified
5 based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *M. catarrhalis* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the present invention, including function-conservative variants
10 of the disclosed ORFs, may be isolated from wild-type or mutant *M. catarrhalis* cells, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) including *M. catarrhalis* into which an *M. catarrhalis* -derived protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

15 *M. catarrhalis* polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, *J. Am. Chem. Soc.* 85:2149.
20 The synthesis is carried out with amino acids that are protected at the alpha-amino terminus. Trifunctional amino acids with labile side-chains are also protected with suitable groups to prevent undesired chemical reactions from occurring during the assembly of the polypeptides. The alpha-amino protecting group is selectively removed to allow subsequent reaction to take place at the amino-terminus. The conditions for the removal of the alpha-
25 amino protecting group do not remove the side-chain protecting groups.

Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant
30 system in which the *M. catarrhalis* protein contains an additional sequence tag that

facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against an *M. catarrhalis* protein or against peptides derived therefrom can be used as purification reagents. Other purification
5 methods are possible.

The present invention also encompasses derivatives and homologues of *M. catarrhalis*-encoded polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more amino
10 acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

The isolated polypeptides may be modified by, for example, phosphorylation,
15 sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

To identify *M. catarrhalis*-derived polypeptides for use in the present invention, essentially the complete genomic sequence of a virulent, methicillin-resistant isolate of *M. catarrhalis* isolate was analyzed. While, in very rare instances, a nucleic acid sequencing
20 error may be revealed, resolving a rare sequencing error is well within the art, and such an occurrence will not prevent one skilled in the art from practicing the invention.

Also encompassed are any *M. catarrhalis* polypeptide sequences that are contained within the open reading frames (ORFs), including complete protein-coding sequences, of
25 which any of SEQ ID NO: 1 - SEQ ID NO: 1920 forms a part. Table 2, which is appended herewith and which forms part of the present specification, provides a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. As a result, one skilled in the art can

use the polypeptides of the present invention for commercial and industrial purposes consistent with the type of putative identification of the polypeptide.

The present invention provides a library of *M. catarrhalis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences that are contemplated for use as components of vaccines. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended herewith and which forms part of the present specification.

The present invention also provides a library of *M. catarrhalis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences lacking homology to any known prokaryotic or eukaryotic sequences. Such libraries provide probes, primers, and markers which can be used to diagnose *M. catarrhalis* infection, including use as markers in epidemiological studies. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended hereto and part hereof.

The present invention also provides a library of *M. catarrhalis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise targets for therapeutic drugs.

SPECIFIC EXAMPLE: DETERMINATION OF *MORAXELLA* PROTEIN ANTIGENS FOR ANTIBODY AND VACCINE DEVELOPMENT

The selection of Moraxella protein antigens for vaccine development can be derived from the nucleic acids encoding *M. catarrhalis* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR
5 databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities lower than 1×10^{-6} that the homology is only due to random chance) to membrane or
exported proteins represent protein antigens for vaccine development. Possible functions
10 can be provided to *M. catarrhalis* genes based on sequence homology to genes cloned in other organisms.

Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid sequence and compares it to information derived from the properties of known
15 membrane and exported proteins. This comparison predicts which proteins will be exported, membrane associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

20 PRODUCTION OF FRAGMENTS AND ANALOGS OF *M. CATARRHALIS* NUCLEIC ACIDS AND POLYPEPTIDES

Based on the discovery of the *M. catarrhalis* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed structure of *M. catarrhalis* genes, e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art
25 which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *M. catarrhalis* polypeptides. Such screens are useful for the identification of inhibitors of *M. catarrhalis*.

GENERATION OF FRAGMENTS

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments. Digestion with "end-nibbling" endonucleases can thus generate DNAs which encode an array of fragments. DNAs which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

ALTERATION OF NUCLEIC ACIDS AND POLYPEPTIDES: RANDOM METHODS

Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

PCR MUTAGENESIS

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of

amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

SATURATION MUTAGENESIS

5 Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all
10 possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

15 DEGENERATE OLIGONUCLEOTIDES

A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang,
20 SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al.
25 (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS* 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

ALTERATION OF NUCLEIC ACIDS AND POLYPEPTIDES: METHODS FOR DIRECTED MUTAGENESIS

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

ALANINE SCANNING MUTAGENESIS

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyalanine). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

OLIGONUCLEOTIDE-MEDIATED MUTAGENESIS

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to

a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least about 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

CASSETTE MUTAGENESIS

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the mutated desired protein subunit DNA sequence.

COMBINATORIAL MUTAGENESIS

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of degenerate sequences.

OTHER MODIFICATIONS OF *M. CATARRHALIS* NUCLEIC ACIDS AND POLYPEPTIDES

It is possible to modify the structure of an *M. catarrhalis* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to proteolytic degradation *in vivo*). A modified *M. catarrhalis* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *M. catarrhalis* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *M. catarrhalis* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *M. catarrhalis* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Schon and co-

workers (Wie et al., supra) to produce a protein conjugated with PEG. In addition, PEG can be added during chemical synthesis of the protein. Other modifications of *M. catarrhalis* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, supra); chemical
5 coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of an *M. catarrhalis* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone.
10 For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

15 To potentially aid proper antigen processing of epitopes within an *M. catarrhalis* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered
20 sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

PRIMARY METHODS FOR SCREENING POLYPEPTIDES AND ANALOGS

25 Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *M. catarrhalis* polypeptide or an interacting protein,
30 facilitates relatively easy isolation of the vector encoding the gene whose product was

detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

TWO HYBRID SYSTEMS

5 Two hybrid assays such as the system described below (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *M. catarrhalis* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *M. catarrhalis* protein. (The *M. catarrhalis* domain is used as the bait protein and the library of variants are expressed as prey fusion
10 proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind an *M. catarrhalis* polypeptide.

DISPLAY LIBRARIES

15 In one approach to screening assays, the Moraxella peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO
20 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to be visually inspected and separated under a fluorescence
25 microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since
30 these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per

milliliter, a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages, M13, fd., and f1, are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 91, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motive organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Ku wajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners. Examples include the *Moraxella* protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull *et al.* (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull *et al.* (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, *et al.* (1990) *Proc. Natl. Acad. Sci. U.S.A.* 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are

confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries. This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries. Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is

recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide
5 expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the
10 sequences of the active peptides one sequences the DNA produced by the phagemid host.

SECONDARY SCREENING OF POLYPEPTIDES AND ANALOGS

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to
15 differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated through one of the primary screens described above.

20 Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

PEPTIDE MIMETICS OF *M. CATARRHALIS* POLYPEPTIDES

25 The invention also provides for reduction of the protein binding domains of the subject *M. catarrhalis* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *M. catarrhalis* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *M. catarrhalis* polypeptide which are involved in molecular
30 recognition of a polypeptide can be determined and used to generate *M. catarrhalis* -derived

peptidomimetics which competitively or noncompetitively inhibit binding of the *M. catarrhalis* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *M. catarrhalis* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *M. catarrhalis* polypeptide to an interacting polypeptide and thereby interfere with the function of *M. catarrhalis* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), b-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and et al. (1986) *Biochem Biophys Res Commun* 134:71).

VACCINE FORMULATIONS FOR *M. CATARRHALIS* NUCLEIC ACIDS AND POLYPEPTIDES

This invention also features vaccine compositions for protection against infection by *M. catarrhalis* or for treatment of *M. catarrhalis* infection. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *M. catarrhalis*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *M. catarrhalis* surface proteins. Any

nucleic acid encoding an immunogenic *M. catarrhalis* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against infection by *M. catarrhalis* which contains at least one immunogenic fragment of an *M. catarrhalis* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *M. catarrhalis* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed

by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *M. catarrhalis* peptide in association with appropriate MHC molecules to T cells in conjunction with the necessary co-stimulation has the effect of transmitting a
5 signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad. Sci USA*,
86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit
10 for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of
15 cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

Vaccine compositions of the invention containing immunogenic components (e.g., *M. catarrhalis* polypeptide or fragment thereof or nucleic acid encoding an *M. catarrhalis* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier.
20 The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of
25 auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *M. catarrhalis* polypeptides, the polypeptide is co-administered with a suitable adjuvant.

It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and pulmonary formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *M. catarrhalis*. Cain et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *M. catarrhalis* polypeptide with cholera toxin or its B subunit, procholeraenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*M. catarrhalis* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immunostimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like

particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 mg to 50 mg, for example 10 mg to 35 mg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *M. catarrhalis* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *M. catarrhalis* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a susceptible host to prevent infection by *M. catarrhalis*. The vaccines of the invention are administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 mg to 10 g, preferably 10 mg to 100 mg. A suitable dosage for adults will also be in the range of 5 mg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a killed whole *E. coli* preparation with an immunogenic fragment of an *M. catarrhalis* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

5 It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *M. catarrhalis* infection, some are useful only for treating *M. catarrhalis* infection, and some are useful for both preventing and treating *M. catarrhalis* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *M. catarrhalis* infection by stimulating humoral and/or cell-
10 mediated immunity against *M. catarrhalis*. It should be understood that amelioration of any of the symptoms of *M. catarrhalis* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *M. catarrhalis*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.-

15 ANTIBODIES REACTIVE WITH *M. CATARRHALIS* POLYPEPTIDES

The invention also includes antibodies specifically reactive with the subject *M. catarrhalis* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster
20 or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *M. catarrhalis* polypeptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or
25 other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *M. catarrhalis* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related
30 human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least

about 95% homologous). In yet a further preferred embodiment of the invention, the anti-*M. catarrhalis* antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most preferred embodiment, there is no cross-reactivity between bacterial and mammalian antigens.

10 The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *M. catarrhalis* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*M. catarrhalis* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *M. catarrhalis* polypeptides or *M. catarrhalis* polypeptide variants, and antibody fragments such as Fab' and F(ab')₂, can be used to block the action of *M. catarrhalis* polypeptide and allow the study of the role of a particular *M. catarrhalis* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *M. catarrhalis* and by microinjection of anti-*M. catarrhalis* polypeptide antibodies of the present invention.

20 Antibodies which specifically bind *M. catarrhalis* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *M. catarrhalis* antigens. Anti-*M. catarrhalis* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *M. catarrhalis* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *M. catarrhalis* polypeptide levels in an individual can allow

determination of the efficacy of a given treatment regimen for an individual afflicted with such a disorder. The level of an *M. catarrhalis* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*M. catarrhalis* antibodies can include, for
5 example, immunoassays designed to aid in early diagnosis of *M. catarrhalis* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *M. catarrhalis* antigens.

Another application of anti-*M. catarrhalis* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as
10 λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *M. catarrhalis* polypeptide can then be detected
15 with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*M. catarrhalis* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *M. catarrhalis* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

20

KITS CONTAINING NUCLEIC ACIDS, POLYPEPTIDES OR ANTIBODIES OF THE INVENTION

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the
25 nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such
30 as particles, supports, wells, dipsticks and the like. Kits may also comprise labeling means

such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to serve their particular purpose. Kits further can include instructions for use.

5

BIO CHIP TECHNOLOGY

The nucleic acid sequence of the present invention may be used to detect *M. catarrhalis* or other species of *Moraxella* acid sequence using bio chip technology. Bio chips containing arrays of nucleic acid sequence can also be used to measure expression of genes of *M. catarrhalis* or other species of *Moraxella*. For example, to diagnose a patient with a *M. catarrhalis* or other *Moraxella* infection, a sample from a human or animal can be used as a probe on a bio chip containing an array of nucleic acid sequence from the present invention. In addition, a sample from a disease state can be compared to a sample from a non-disease state which would help identify a gene that is up-regulated or expressed in the disease state. This would provide valuable insight as to the mechanism by which the disease manifests. Changes in gene expression can also be used to identify critical pathways involved in drug transport or metabolism, and may enable the identification of novel targets involved in virulence or host cell interactions involved in maintenance of an infection. Procedures using such techniques have been described by Brown *et al.*, 1995, *Science* 270: 467-470.

Bio chips can also be used to monitor the genetic changes of potential therapeutic compounds including, deletions, insertions or mismatches. Once the therapeutic is added to the patient, changes to the genetic sequence can be evaluated for its efficacy. In addition, the nucleic acid sequence of the present invention can be used to determine essential genes in cell cycling. As described in Iyer *et al.*, 1999 (*Science*, 283:83-87) genes essential in the cell cycle can be identified using bio chips. Furthermore, the present invention provides nucleic acid sequence which can be used with bio chip technology to understand regulatory networks in bacteria, measure the response to environmental signals or drugs as in drug screening, and study virulence induction. (Mons *et al.*, 1998, *Nature Biotechnology*, 16: 45-48. Patents teaching this technology include U.S. Patents 5445934, 5744305, and 5800992.

DRUG SCREENING ASSAYS USING *M. CATARRHALIS* POLYPEPTIDES

By making available purified and recombinant *M. catarrhalis* polypeptides, the present invention provides assays which can be used to screen for drugs which are either
5 agonists or antagonists of the normal cellular function, in this case, of the subject *M. catarrhalis* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *M. catarrhalis* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the person skilled in the art.

10 In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively
15 easy detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target.
20 Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *M. catarrhalis* polypeptide.

Screening assays can be constructed *in vitro* with a purified *M. catarrhalis* polypeptide or fragment thereof, such as an *M. catarrhalis* polypeptide having enzymatic activity, such that the activity of the polypeptide produces a detectable reaction product. The
25 efficacy of the compound can be assessed by generating dose response curves from data obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring
30 compounds can be tested in the assay to identify those which inhibit or potentiate the activity

of the *M. catarrhalis* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *M. catarrhalis* cells.

5 OVEREXPRESSION ASSAYS

Overexpression assays are based on the premise that overproduction of a protein would lead to a higher level of resistance to compounds that selectively interfere with the function of that protein. Overexpression assays may be used to identify compounds that interfere with the function of virtually any type of protein, including without limitation
10 enzymes, receptors, DNA- or RNA-binding proteins, or any proteins that are directly or indirectly involved in regulating cell growth.

Typically, two bacterial strains are constructed. One contains a single copy of the gene of interest, and a second contains several copies of the same gene. Identification of useful inhibitory compounds of this type of assay is based on a comparison of the activity of
15 a test compound in inhibiting growth and/or viability of the two strains. The method involves constructing a nucleic acid vector that directs high level expression of a particular target nucleic acid. The vectors are then transformed into host cells in single or multiple copies to produce strains that express low to moderate and high levels of protein encoding by the target sequence (strain A and B, respectively). Nucleic acid comprising sequences
20 encoding the target gene can, of course, be directly integrated into the host cell.

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on the growth of the two strains. Agents which interfere with an unrelated target equally inhibit the growth of both strains. Agents which interfere with the function of the target at high concentration should inhibit the growth of
25 both strains. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit the growth of strain A at a concentration of the compound that allows strain B to grow.

Alternatively, a bacterial strain is constructed that contains the gene of interest under
30 the control of an inducible promoter. Identification of useful inhibitory agents using this

type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of this strain under both inducing and non-inducing conditions. The method involves constructing a nucleic acid vector that directs high-level expression of a particular target nucleic acid. The vector is then transformed into host cells that are grown
5 under both non-inducing and inducing conditions (conditions A and B, respectively).

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on growth under these two conditions. Agents that interfere with the function of the target should inhibit growth under both conditions. It should be possible, however, to titrate out the inhibitory effect of the compound in the
10 overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit growth under condition A at a concentration that allows the strain to grow under condition B.

LIGAND-BINDING ASSAYS

15 Many of the targets according to the invention have functions that have not yet been identified. Ligand-binding assays are useful to identify inhibitor compounds that interfere with the function of a particular target, even when that function is unknown. These assays are designed to detect binding of test compounds to particular targets. The detection may involve direct measurement of binding. Alternatively, indirect indications of binding may
20 involve stabilization of protein structure or disruption of a biological function. Non-limiting examples of useful ligand-binding assays are detailed below.

A useful method for the detection and isolation of binding proteins is the Biomolecular Interaction Assay (BIAcore) system developed by Pharmacia Biosensor and described in the manufacturer's protocol (LKB Pharmacia, Sweden). The BIAcore system
25 uses an affinity purified anti-GST antibody to immobilize GST-fusion proteins onto a sensor chip. The sensor utilizes surface plasmon resonance which is an optical phenomenon that detects changes in refractive indices. In accordance with the practice of the invention, a protein of interest is coated onto a chip and test compounds are passed over the chip. Binding is detected by a change in the refractive index (surface plasmon resonance).

A different type of ligand-binding assay involves scintillation proximity assays (SPA, described in U.S. Patent No. 4,568,649).

Another type of ligand binding assay, also undergoing development, is based on the fact that proteins containing mitochondrial targeting signals are imported into isolated mitochondria *in vitro* (Hurt *et al.*, 1985, *Embo J.* 4:2061-2068; Eilers and Schatz, *Nature*, 1986, 322:228-231). In a mitochondrial import assay, expression vectors are constructed in which nucleic acids encoding particular target proteins are inserted downstream of sequences encoding mitochondrial import signals. The chimeric proteins are synthesized and tested for their ability to be imported into isolated mitochondria in the absence and presence of test compounds. A test compound that binds to the target protein should inhibit its uptake into isolated mitochondria *in vitro*.

Another ligand-binding assay is the yeast two-hybrid system (Fields and Song, 1989, *Nature* 340:245-246). The yeast two-hybrid system takes advantage of the properties of the GAL4 protein of the yeast *Saccharomyces cerevisiae*. The GAL4 protein is a transcriptional activator required for the expression of genes encoding enzymes of galactose utilization. This protein consists of two separable and functionally essential domains: an N-terminal domain which binds to specific DNA sequences (UAS_G); and a C-terminal domain containing acidic regions, which is necessary to activate transcription. The native GAL4 protein, containing both domains, is a potent activator of transcription when yeast are grown on galactose media. The N-terminal domain binds to DNA in a sequence-specific manner but is unable to activate transcription. The C-terminal domain contains the activating regions but cannot activate transcription because it fails to be localized to UAS_G. In the two-hybrid system, a system of two hybrid proteins containing parts of GAL4: (1) a GAL4 DNA-binding domain fused to a protein 'X' and (2) a GAL4 activation region fused to a protein 'Y'. If X and Y can form a protein-protein complex and reconstitute proximity of the GAL4 domains, transcription of a gene regulated by UAS_G occurs. Creation of two hybrid proteins, each containing one of the interacting proteins X and Y, allows the activation region of UAS_G to be brought to its normal site of action.

The binding assay described in Fodor *et al.*, 1991, *Science* 251:767-773, which involves testing the binding affinity of test compounds for a plurality of defined polymers synthesized on a solid substrate, may also be useful.

Compounds which bind to the polypeptides of the invention are potentially useful as
5 antibacterial agents for use in therapeutic compositions.

Pharmaceutical formulations suitable for antibacterial therapy comprise the antibacterial agent in conjunction with one or more biologically acceptable carriers. Suitable biologically acceptable carriers include, but are not limited to, phosphate-buffered saline, saline, deionized water, or the like. Preferred biologically acceptable carriers are
10 physiologically or pharmaceutically acceptable carriers.

The antibacterial compositions include an antibacterial effective amount of active agent. Antibacterial effective amounts are those quantities of the antibacterial agents of the present invention that afford prophylactic protection against bacterial infections or which result in amelioration or cure of an existing bacterial infection. This antibacterial effective
15 amount will depend upon the agent, the location and nature of the infection, and the particular host. The amount can be determined by experimentation known in the art, such as by establishing a matrix of dosages and frequencies and comparing a group of experimental units or subjects to each point in the matrix.

The antibacterial active agents or compositions can be formed into dosage unit forms,
20 such as for example, creams, ointments, lotions, powders, liquids, tablets, capsules, suppositories, sprays, aerosols or the like. If the antibacterial composition is formulated into a dosage unit form, the dosage unit form may contain an antibacterial effective amount of active agent. Alternatively, the dosage unit form may include less than such an amount if multiple dosage unit forms or multiple dosages are to be used to administer a total dosage of
25 the active agent. Dosage unit forms can include, in addition, one or more excipient(s), diluent(s), disintegrant(s), lubricant(s), plasticizer(s), colorant(s), dosage vehicle(s), absorption enhancer(s), stabilizer(s), bactericide(s), or the like.

For general information concerning formulations, see, e.g., Gilman et al. (eds.), 1990, *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*, 8th ed., Pergamon
30 Press; and *Remington's Pharmaceutical Sciences*, 17th ed., 1990, Mack Publishing Co.,

Easton, PA; Avis et al. (eds.), 1993, *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York; Lieberman et al (eds.), 1990, *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York.

5 The antibacterial agents and compositions of the present invention are useful for preventing or treating *M. catarrhalis* infections. Infection prevention methods incorporate a prophylactically effective amount of an antibacterial agent or composition. A prophylactically effective amount is an amount effective to prevent *M. catarrhalis* infection and will depend upon the specific bacterial strain, the agent, and the host. These amounts can be determined experimentally by methods known in the art and as described above.

10 *M. catarrhalis* infection treatment methods incorporate a therapeutically effective amount of an antibacterial agent or composition. A therapeutically effective amount is an amount sufficient to ameliorate or eliminate the infection. The prophylactically and/or therapeutically effective amounts can be administered in one administration or over repeated administrations. Therapeutic administration can be followed by prophylactic administration, 15 once the initial bacterial infection has been resolved.

The antibacterial agents and compositions can be administered topically or systemically. Topical application is typically achieved by administration of creams, ointments, lotions, or sprays as described above. Systemic administration includes both oral and parental routes. Parental routes include, without limitation, subcutaneous, 20 intramuscular, intraperitoneal, intravenous, transdermal, inhalation and intranasal administration.

EXEMPLIFICATION

25 CLONING AND SEQUENCING *M. CATARRHALIS* GENOMIC SEQUENCE

This invention provides nucleotide sequences of the genome of *M. catarrhalis* which thus comprises a DNA sequence library of *M. catarrhalis* genomic DNA. The invention also provides nucleotide sequences of two naturally occurring plasmids in *M. catarrhalis*. The detailed description that follows provides nucleotide sequences of *M. catarrhalis*, and also 30 describes how the sequences were obtained and how ORFs (Open Reading Frames) and

protein-coding sequences can be identified. Also described are methods of using the disclosed *M. catarrhalis* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *M. catarrhalis* as well as other species of *Moraxella*.

Chromosomal DNA from strain 98-4362. of *M. catarrhalis*, was isolated using a protocol described by Storrs, et al. (*J. Bacteriol.* 173: 4347-4352 (1991)). The only exception to this protocol was that lysostaphin (120 U/ml) was used instead of lysozyme. The genomic DNA prep involved a lysozyme:lysostaphin digestion, sodium dodecyl sulfate lysis, Proteinase K and RNase treatment, phenol:chloroform extraction, and sodium acetate precipitation, followed by the CsCl gradient to remove the plasmid.

In the construction of both libraries, genomic *M. catarrhalis* DNA was hydrodynamically sheared in an HPLC and then separated on a standard 1% agarose gel. A fraction corresponding to 2000-3000 bp in length was excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adapters (5'-GTCTTCACCACGGGG-3' and 5'-GTGGTGAAGAC-3' in 100-1000 fold molar excess). These linkers are complimentary to the BstXI-cut pGTC vector, while the overhang is not self-complimentary. Therefore, the linkers will not concatamerize nor will the cut-vector religate itself easily. The linker-adapted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adapted inserts were then ligated to BstXI-cut vector to construct a "shotgun" subclone libraries.

Only major modifications to the protocols are highlighted. Briefly, the library was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Transformants were then used for plating of clones and picking for sequencing. The cultures were grown overnight at 37°C. DNA was purified using a silica bead DNA preparation (Engelstein, 1996) method. In this manner, 25 μ g of DNA was obtained per clone.

These purified DNA samples were then sequenced using primarily ABI dye-terminator chemistry. All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The ABI dye terminator sequence reads were run on ABI377 machines and the data was transferred to UNIX machines following lane tracking of the gels. Base calls and quality scores were determined using the program PHRED (Ewing et al., 1998, Genome Res. 8: 175-185; Ewing and Green, 1998, Genome Res. 8: 685-734). Reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157) with default program parameters and quality scores.

Finishing followed the initial assembly. Missing mates (sequences from clones that only gave reads from one end of the *Moraxella* DNA inserted in the plasmid) were identified and sequenced with ABI technology to allow the identification of additional overlapping contigs.

End-sequencing of randomly picked genomic lambda was also performed. Sequencing of both sides was done for all lambda sequences. The lambda library backbone helped to verify the integrity of the assembly and allowed closure of some of the physical gaps. Primers for walking off the ends of contigs would be selected using pick_primer (a GTC program) near the ends of the clones to facilitate gap closure. These walks can be sequenced using the selected clones and primers. These data are then reassembled with PHRAP. Additional sequencing using PCR-generated templates and screened and/or unscreened lambda templates can be done in addition.

Additional templates for the physical gaps were obtained through PCR using primers designed from the ends of the contigs. These templates were then used in sequencing reactions to close the gaps.

Contigs were ordered by aligning identified *M. catarrhalis* genes to the published physical maps. Order was confirmed by PCR. The final chromosomal assembly included 119 contigs.

To identify *M. catarrhalis* polypeptides the complete genomic sequence of *M. catarrhalis* were analyzed essentially as follows: First, all possible stop-to-stop open reading frames (ORFs) greater than 180 nucleotides in all six reading frames were translated into amino acid sequences. Second, the identified ORFs were analyzed for homology to known
5 (archaeobacter, prokaryotic and eukaryotic) protein sequences. Third, the coding potential of non-homologous sequences were evaluated with the program GENEMARK™ (Borodovsky and McIninch, 1993, Comp. Chem. 17:123)

10 IDENTIFICATION, CLONING AND EXPRESSION OF *M. CATARRHALIS* NUCLEIC ACIDS

Expression and purification of the *M. catarrhalis* polypeptides of the invention can be performed essentially as outlined below.

To facilitate the cloning, expression and purification of membrane and secreted proteins from *M. catarrhalis*, a gene expression system, such as the pET System (Novagen),
15 for cloning and expression of recombinant proteins in *E. coli*, is selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, is fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end is selected for fusion in order to avoid alteration of any 5' terminal signal sequence.

20 PCR AMPLIFICATION AND CLONING OF NUCLEIC ACIDS CONTAINING ORF'S ENCODING ENZYMES

Nucleic acids chosen (for example, from the nucleic acids set forth in SEQ ID NO: 1 - SEQ ID NO: 2501 for cloning from the 98-4362. strain of *M. catarrhalis* and plasmids are prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic
25 oligonucleotide primers specific for the 5' and 3' ends of open reading frames (ORFs) are designed and purchased from GibcoBRL Life Technologies (Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) are designed to include an NcoI cloning site at the extreme 5' terminus. These primers are designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding

sequence for the remainder of the native *M. catarrhalis* DNA sequence. All reverse primers (specific for the 3' end of any *M. catarrhalis* ORF) include a EcoRI site at the extreme 5' terminus to permit cloning of each *M. catarrhalis* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids including six histidine residues (at the extreme C-terminus), which
5 comprise the His-Tag.

Genomic DNA or plasmid DNA prepared from the 98-4362. strain of *M. catarrhalis* is used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a
10 DNA sequence containing an *M. catarrhalis* ORF, genomic DNA (50 nanograms) is introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *M. catarrhalis* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular
15 Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters.

Upon completion of thermal cycling reactions, each sample of amplified DNA is washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples are subjected to digestion with the restriction endonucleases, e.g., NcoI and EcoRI (New England BioLabs, Beverly, MA, USA)(Current
20 Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples are then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA is visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel is purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

25

CLONING OF *M. CATARRHALIS* NUCLEIC ACIDS INTO AN EXPRESSION VECTOR

The pET-28b vector is prepared for cloning by digestion with restriction endonucleases, e.g., NcoI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). The pET-28a vector, which encodes a His-Tag

that can be fused to the 5' end of an inserted gene, is prepared by digestion with appropriate restriction endonucleases.

Following digestion, DNA inserts are cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously
5 digested pET-28b expression vector. Products of the ligation reaction are then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) as described below.

10 TRANSFORMATION OF COMPETENT BACTERIA WITH RECOMBINANT PLASMIDS

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), are transformed with recombinant pET expression plasmids carrying the cloned *M. catarrhalis* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction is mixed with 50
15 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples are incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples are then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 are
20 then picked and analyzed to evaluate cloned inserts as described below.

IDENTIFICATION OF RECOMBINANT EXPRESSION VECTORS WITH *M. CATARRHALIS* NUCLEIC ACIDS

Individual BL21 clones transformed with recombinant pET-28b *M. catarrhalis* ORFs
25 are analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *M. catarrhalis* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verifies the integration of the *M. catarrhalis* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

30

ISOLATION AND PREPARATION OF NUCLEIC ACIDS FROM TRANSFORMANTS

Individual clones of recombinant pET-28b vectors carrying properly cloned *M. catarrhalis* ORFs are picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA is isolated and purified using
5 the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

EXPRESSION OF RECOMBINANT *M. CATARRHALIS* SEQUENCES IN *E. COLI*

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression
10 include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase. These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used
15 include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *M. catarrhalis* sequences, 50 nanograms of plasmid DNA isolated as described above is used to transform competent BL21(DE3) bacteria as described above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-
20 galactosidase) is expressed in the pET-System as described for the *M. catarrhalis* recombinant constructions. Transformed cells are cultured in SOC medium for 1 hour, and the culture is then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies are pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D. units, at which
25 point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *M. catarrhalis* recombinant DNA constructions .

After induction of gene expression with IPTG, bacteria are pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4⁰ C. Pellets are resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE

buffer). Cells are then centrifuged at 2000 x g for 20 min at 4⁰ C. Wet pellets are weighed and frozen at -80⁰ C until ready for protein purification.

A variety of methodologies known in the art can be utilized to purify the isolated proteins. (Current Protocols in Protein Science, John Wiley and Sons, Inc., J. E. Coligan et al., eds., 1995). For example, the frozen cells may be thawed, resuspended in buffer and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate may be centrifuged to yield a clear supernatant (crude extract) and following filtration the crude extract may be fractionated over columns. Fractions may be monitored by absorbance at OD₂₈₀ nm. and peak fractions may analyzed by SDS-PAGE

The concentrations of purified protein preparations may be quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations are also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels of various concentrations may be purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers may include rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

25 EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments and methods described herein. The specific embodiments described herein are offered by way of example

only, and the invention is to limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled.

TABLE 2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2538928_c3_3	1	1921	84	255	306	3.3e-27

Protein name

Locus Name

Acc#

sp:ETFA_HUMAN

P13804

Description

ELECTRON TRANSFER FLAVOPROTEIN ALPHA-SUBUNIT PRECURSOR (ALPHA-ETF)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24035192_f2_1	2	1922	502	1509	138	1.5e-05

Protein name

Locus Name

Acc#

icmF protein

pir:T18341

T18341

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10547151_c1_2	3	1923	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24317313_c2_2	4	1924	201	606	316	3.2e-27

Protein name

Locus Name

Acc#

sp:SYFB_HAEIN

P43820

Description

TRNA LIGASE BETA CHAIN) (PHERS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11911687_c2_42	5	1925	284	855	709	6.5e-70

Protein name

Locus Name

Acc#

3-methyl-2-oxobutanoate

gp:PFL130846

AJ130846

Description

Pseudomonas fluorescens folk (partial), panB and panC (partial) genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14334452_c2_44	6	1926	221	666	339	2.9e-35

Protein name

Locus Name

Acc#

gp:ECHSDMSR

X13145

Description

Escherichia Coli plasmid R124/3 hsdM, hsdS and hsdR genes for EcoR124/3 type I restriction and modification enzyme.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16619747_c3_48	7	1927	73	222	158	1.6e-11

Protein name

Locus Name

Acc#

sp:YBAV_HAEIN

Q57134

Description

HYPOTHETICAL PROTEIN HI1008

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21657635_f3_22	8	1928	221	666	381	3.7e-35

Protein name

Locus Name

Acc#

sp:DSBA_PSEAE

P95460

Description

THIOL:DISULFIDE INTERCHANGE PROTEIN DSBA PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23476431_c3_54	9	1929	181	546	123	3.8e-07

Protein name

Locus Name

Acc#

sp:YJGA_HAEIN

P45076

Description

HYPOTHETICAL PROTEIN HI1151

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23945165_c3_49	10	1930	170	513	334	3.6e-30

Protein name

Locus Name

Acc#

2-amino-4-hydroxy-6-hydroxymethyldihydropteridine

pir:C64046

C64046

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24351555_c2_38	11	1931	130	393	135	1.0e-08

Protein name

Locus Name

Acc#

sp:MAZG_HAEIN

P44723

Description

MAZG PROTEIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2835152_f2_14	12	1932	82	249		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34178802_c2_45	13	1933	132	399	184	3.3e-14

Protein name

Locus Name

Acc#

conserved hypothetical secreted protein
HP1098

pir:B64657

B64657

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35819090_c1_31	14	1934	623	1872	689	8.5e-68

Protein name

Locus Name

Acc#

polynucleotide adenylyltransferase

gp:PPY18131

Y18131

Description

Pseudomonas putida pcnB gene and partial folk gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4468761_f2_18	15	1935	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4492138_c2_43	16	1936	283	852	660	1.0e-64

Protein name

Locus Name

Acc#

sp:PANC_SCHPO

Q09673

Description

SYNTHETASE) (PANTOATE ACTIVATING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
48796812_c3_47	17	1937	84	255	138	1.8e-08

Protein name

Locus Name

Acc#

sp:CBF5_YEAST

P33322

Description

5) (NUCLEOLAR PROTEIN CBF5) (P64')

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5110943_c1_32	18	1938	298	897	604	8.7e-59

Protein name

Locus Name

Acc#

gp:AB033988

AB033988

Description

Shewanella violacea gene for RpoN(sigma54), nitrogen regulatory II A protein, phosphocarrier protein NPR, hypothetical proteins, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5112807_c3_52	19	1939	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26285938_f1_1	20	1940	207	624	541	4.1e-52

Protein name

Locus Name

Acc#

sp:YCEG_HAEIN

P44720

Description

HYPOTHETICAL PROTEIN HI0457

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30658587_f1_2	21	1941	73	219	126	4.8e-08

Protein name

Locus Name

Acc#

sp:KTHY_BACSU

P37537

Description

THYMIDYLATE KINASE, (DTMP KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2767080_f1_2	22	1942	373	1122	1522	4.6e-156

Protein name

Locus Name

Acc#

sp:EFTU_SHEPU

P33169

Description

ELONGATION FACTOR TU (EF-TU)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32110007_c2_8	23	1943	88	267	114	7.3e-07

Protein name

Locus Name

Acc#

hypothetical protein PH1485

pir:H71023

H71023

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36329582_c1_5	24	1944	60	183	144	5.5e-09

Protein name

Locus Name

Acc#

sp:YHA2_EIKCO

P35649

Description

HYPOTHETICAL 66.3 KD PROTEIN IN HAG2 5'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
971016_f1_1	25	1945	198	597	643	6.4e-63

Protein name

Locus Name

Acc#

sp:EFG_HELPY

P56002

Description

ELONGATION FACTOR G (EF-G)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2225312_f3_18	26	1946	427	1284	416	1.9e-64

Protein name

glycerophosphoryl diester phosphodiesterase

Locus Name

pir:D75630

Acc#

D75630

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23457692_f1_1	27	1947	392	1179	360	1.9e-42

Protein name

Locus Name

sp:RECF_PSEPU

Acc#

P13456

Description

RECF PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26042927_f3_19	28	1948	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26750837_f1_4	29	1949	111	336	202	4.9e-16

Protein name

hypothetical protein

Locus Name

pir:S76551

Acc#

S76551

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36144675_f1_2	30	1950	525	1578	1851	6.3e-191

Protein name

Locus Name

sp:GUAA_HAEIN

Acc#

P44335

Description

AMIDOTRANSFERASE) (GMP SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4298443_f2_8	31	1951	822	2469	2597	5.6e-270

Protein name

Locus Name

Acc#

sp:GYRB_ECOLI

Description

P06982:008
438

DNA GYRASE SUBUNIT B,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12617627_c1_1	32	1952	128	387	650	1.2e-63

Protein name

Locus Name

Acc#

transposase

pir:167760

167760

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34175180_c2_2	33	1953	90	273	137	1.7e-08

Protein name

Locus Name

Acc#

transposase

gp:AB026428

AB026428

Description

Methylomonas aminofaciens ribulose monophosphate pathway genes(rmpD, rmpA, IS10-R rmpI, rmpB), complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16690875_f1_2	34	1954	82	249	90	0.00026

Protein name

Locus Name

Acc#

TolR protein

gp:PPPAL1

X74218

Description

Pseudomonas putida ruvB, tolQ, tolR, tolA, tolB and oprL genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1953953_c2_15	35	1955	534	1605	1387	9.3e-142

Protein name

Locus Name

Acc#

sp:ANIA_NEIGO

Q02219

Description

MAJOR OUTER MEMBRANE PROTEIN PAN 1 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22667557_f2_6	36	1956	177	534	260	4.5e-31

Protein name

Locus Name

Acc#

sp:YHDE_BACSU

007573

Description

HYPOTHETICAL 16.6 KD PROTEIN IN GLPD-SPOVR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30644217_f2_8	37	1957	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4881533_f2_7	38	1958	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6651712_f2_2	39	1959	271	816	611	1.6e-59

Protein name

Locus Name

Acc#

isocitrate lyase

gp:AB004651

AB004651

Description

Hyphomicrobium methylovorum gene for isocitrate lyase, inorganic phosphate transporter, methionine synthase, complete and partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14647952_f1_1	40	1960	912	2739	2108	3.7e-218

Protein name

Locus Name

Acc#

initiation factor IF2-alpha

gp:PVAJ2737

AJ002737

Description

Proteus vulgaris infB gene and partial nuaA and rbfA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
15032818_c1_15	41	1961	172	519	112	4.1e-05

Protein name

hypothetical protein

Locus Name

pir:G75410

Acc#

G75410

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21644075_c1_14	42	1962	199	600	381	3.7e-35

Protein name

conserved hypothetical protein

Locus Name

pir:F75410

Acc#

F75410

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24650277_f1_3	43	1963	312	939	543	2.5e-52

Protein name

Locus Name

sp:TRUB_HAEIN

Acc#

P45142

Description

HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3332760_f2_11	44	1964	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3407812_f2_9	45	1965	168	507	215	1.4e-17

Protein name

Locus Name

sp:RBFA_ECOLI

Acc#

P09170

Description

RIBOSOME-BINDING FACTOR A (P15B PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4573462_c2_24	46	1966	103	312	171	2.0e-12

Protein name

conserved hypothetical protein

Locus Name

pir:F75410

Acc#

F75410

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4968825_f2_5	47	1967	217	654	466	3.7e-44

Protein name

Locus Name

sp:NUSA_ECOLI

Acc#

P03003

Description

N UTILIZATION SUBSTANCE PROTEIN A (NUSA PROTEIN) (L FACTOR)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7070265_f1_4	48	1968	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4143942_f3_1	49	1969	319	957	164	1.1e-11

Protein name

hypothetical protein b1759

Locus Name

pir:G64935

Acc#

G64935

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1072952_f3_19	50	1970	331	996	281	2.5e-24

Protein name

Locus Name

sp:SUG2_YEAST

Acc#

P53549:Q08
718

Description

PROBABLE 26S PROTEASE SUBUNIT SUG2 (PROTEASOMAL CAP SUBUNIT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
112880_f1_4	51	1971	99	300	120	1.7e-07

Protein name

hypothetical protein APE2554

Locus Name

pir:C72489

Acc#

C72489

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14633260_f2_12	52	1972	167	504		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19532782_c2_33	53	1973	513	1542	1454	7.4e-149

Protein name

Locus Name

Acc#

sp:TRPE_ACICA

P23315

Description

ANTHRANILATE SYNTHASE COMPONENT I,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20939567_f1_1	54	1974	138	417		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22070965_f2_11	55	1975	123	372	88	0.018

Protein name

Locus Name

Acc#

alanine--tRNA ligase, alaS:alanyl-tRNA
synthetase:alanyl-tRNA synthetase

pir:D70127

D70127

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23839667_c1_25	56	1976	318	957	732	2.4e-72

Protein name

Locus Name

Acc#

sp:DAPA_HAETN

P43797

Description

DIHYDRODIPICOLINATE SYNTHASE, (DHDPS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26281300_c3_35	57	1977	119	360	257	5.1e-22

Protein name

Locus Name

Acc#

sp:Y01B_MYCTU

Q10514

Description

HYPOTHETICAL 39.6 KD PROTEIN CY427.11C

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30507291_f3_20	58	1978	174	525		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4792250_c1_26	59	1979	114	345		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5282805_c3_34	60	1980	241	726	786	4.5e-78

Protein name

Locus Name

Acc#

sp:PUR7_ECOLI

P21155

Description

(SAICAR SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24020430_f2_1	61	1981	127	381	649	1.5e-63

Protein name

transposase

Locus Name

pir:I67760

Acc#

I67760

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
129813_f2_1	62	1982	126	381		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4391518_f2_4	63	1983	64	195	108	3.2e-06

Protein name

Locus Name

Acc#

sp:THIX_HAEIN

P43787

Description

THIOREDOXIN-LIKE PROTEIN HI1115

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4495268_f2_2	64	1984	110	333	512	4.9e-49

Protein name

ferredoxin [3Fe-4S

Locus Name

pir:FEAV

Acc#

A29936:A00
218

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4860875_f3_6	65	1985	159	480	204	2.1e-16

Protein name

hypothetical protein APE2447

Locus Name

pir:F72475

Acc#

F72475

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15677200_f2_2	66	1986	158	477	428	3.9e-40

Protein name

Locus Name

Acc#

sp:CYSW_ECOLI

Description

P16702:P76

534

SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYSW

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4490678_f1_1	67	1987	247	741	643	6.4e-63

Protein name

Locus Name

Acc#

sp:CYSA_ECOLI

Description

P16676:P77

693

SULFATE TRANSPORT ATP-BINDING PROTEIN CYSA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16054077_f3_20	68	1988	520	1563		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16495465_f1_1	69	1989	77	234	72	0.020

Protein name

Locus Name

Acc#

sp:YDIE_ECOLI

P40721

Description

HYPOTHETICAL 7.1 KD PROTEIN IN AROH-NLPC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23485750_c3_36	70	1990	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23730017_c1_24	71	1991	947	2844	278	2.2e-36

Protein name

Locus Name

Acc#

sp:YTFM_HAEIN

P44038

Description

HYPOTHETICAL PROTEIN HI0698 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23859387_f2_14	72	1992	296	891	93	0.048

Protein name

Locus Name

Acc#

conserved hypothetical protein yrrB

pir:H69978

H69978

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34119002_f3_18	73	1993	444	1335	714	1.1e-69

Protein name

Locus Name

Acc#

2-acylglycerophosphoethanolamine
acyltransferase (aas) RP620

pir:E71667

E71667

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4480217_c3_35	74	1994	1675	5028	678	1.5e-79

Protein name

Locus Name

Acc#

sp:YTFN_HAEIN

Q57523

Description

HYPOTHETICAL PROTEIN HI0696

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12378407_c2_32	75	1995	278	834	626	4.1e-61

Protein name

Locus Name

Acc#

sp:PDXJ_ECOLI

P24223

Description

PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN PDXJ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14487952_f1_7	76	1996	72	219		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
161402_c2_29	77	1997	61	186	59	0.018

Protein name Locus Name Acc#

envelope glycoprotein gp:HIVU90070 U90070

Description

HIV-1 strain VN16 from Vietnam, envelope glycoprotein V3 region(env) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16171905_c2_28	78	1998	67	204		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22324331_f2_16	79	1999	77	234		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22463311_f3_22	80	2000	103	312		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23442503_c2_31	81	2001	346	1041	831	7.7e-83

Protein name

Era

Locus Name

gp:AF123492

Acc#

AF123492

Description

Pseudomonas aeruginosa rnc-era-recO operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24412781_c3_34	82	2002	101	306		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26570925_c2_30	83	2003	268	807	500	9.1e-48

Protein name

Locus Name

Acc#

sp:RNC_ECOLI

P05797:P06141

Description

RIBONUCLEASE III, (RNASE III)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26678567_c1_24	84	2004	63	192	88	0.00042

Protein name

Locus Name

Acc#

hypothetical protein 29.1

pir:S59084

S59084

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35161562_c1_27	85	2005	212	639	103	0.0015

Protein name

Locus Name

Acc#

RecO

gp:AF123492

AF123492

Description

Pseudomonas aeruginosa rnc-era-recO operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4063308_c3_35	86	2006	607	1824	2257	5.9e-234

Protein name

Locus Name

Acc#

sp:LEPA_HAEIN

P43729

Description

GTP-BINDING PROTEIN LEPA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4100003_f3_20	87	2007	159	480	624	6.6e-61

Protein name

Locus Name

Acc#

sp:Y882_HAEIN

P44068

Description

HYPOTHETICAL PROTEIN HI0882

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7032838_c3_36	88	2008	367	1104	276	2.0e-44

Protein name

Locus Name

Acc#

signal peptidase I

gp:ECOK12RIII

D64044

Description

Escherichia coli ribonuclease III and other genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9869702_f3_21	89	2009	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10802330_f3_20	90	2010	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12714056_c1_22	91	2011	377	1134	1472	9.1e-151

Protein name putative formaldehyde dehydrogenase Locus Name gp:PSP243941 Acc# AJ243941

Description

Pseudomonas sp. strain HR199 partial vanB, fdh, gcs, ehyA and ehyB genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14844626_c2_34	92	2012	202	609	93	0.028

Protein name transcription regulator, TetR family Locus Name pir:F75482 Acc# F75482

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15705056_c1_24	93	2013	72	219		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
159667_c2_31	94	2014	67	204		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30079512_f3_17	95	2015	76	231	87	0.00053

Protein name Locus Name sp:FIXS_RHIME Acc# P18399

Description

NITROGEN FIXATION PROTEIN FIXS

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35578402_f2_7	96	2016	441	1326	1116	4.8e-113

Protein name

Locus Name

Acc#

sp:YEEF_ECOLI

P33016

Description

HYPOTHETICAL 49.8 KD TRANSPORT PROTEIN IN SBCB-HISL INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3910876_f3_16	97	2017	501	1506	742	2.1e-73

Protein name

Locus Name

Acc#

sp:YDIU_ECOLI

P77649:P76904

Description

HYPOTHETICAL 54.4 KD PROTEIN IN AROH-NLPC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5097812_c2_30	98	2018	120	363	280	1.9e-24

Protein name

Locus Name

Acc#

sp:YAIM_ECOLI

P51025:P77317

Description

HYPOTHETICAL 31.4 KD PROTEIN IN MHPT-ADHC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5210318_f2_10	99	2019	289	870	196	1.5e-15

Protein name

Locus Name

Acc#

hypothetical protein HP0861

pir:E64627

E64627

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6740877_f3_15	100	2020	406	1221	639	1.7e-62

Protein name

Locus Name

Acc#

stearoyl-CoA desaturase

gp:AF026401

AF026401

Description

Mucor rouxii stearoyl-CoA desaturase (Ole1) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
994001_c1_23	101	2021	176	531	573	1.7e-55

Protein name

Locus Name

Acc#

sp:YEIG_ECOLI

P33018

Description

HYPOTHETICAL 31.3 KD PROTEIN IN FOLE-CIRA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1048137_c3_65	102	2022	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10585925_f1_2	103	2023	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14885910_c2_51	104	2024	86	258	71	0.026

Protein name

Locus Name

Acc#

PagK

gp:AF013775

AF013775

Description

Salmonella typhimurium PagK (pagK), PagM (pagM), and PagO (pagO) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22554587_c3_57	105	2025	159	480	480	1.2e-45

Protein name

Locus Name

Acc#

sp:SMPB_ECOLI

P32052:P77
011

Description

SMALL PROTEIN B (18.3 KD PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23437838_f3_28	106	2026	725	2178	1684	3.1e-173

Protein name

Locus Name

Acc#

sp:DNLJ_HAEIN

P43813

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23468813_f3_22	107	2027	309	930	294	6.2e-26

Protein name

Locus Name

Acc#

putative permease BitE

gp:SHU75349

U75349

Description

Serpulina hyodysenteriae bit operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
234807_f1_11	108	2028	175	528	456	4.2e-43

Protein name

Locus Name

Acc#

lipopolysaccharide core biosynthesis protein
kdtB homolog

pir:S72166

S72166

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23705040_f2_16	109	2029	360	1083	670	8.8e-66

Protein name

Locus Name

Acc#

sp:POTA_HAEIN

P45171

Description

SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23726687_f2_17	110	2030	335	1008	745	9.9e-74

Protein name

Locus Name

Acc#

conserved hypothetical protein yddN

pir:F69776

F69776

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23884387_c1_37	111	2031	219	660		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24252305_f2_19	112	2032	298	897	155	8.2e-09

Protein name

Locus Name

Acc#

sp:YDFC_BACSU

P96680

Description

HYPOTHETICAL 33.6 KD PROTEIN IN CSPC-NAP INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24797312_f1_4	113	2033	275	828	132	5.0e-06

Protein name

Locus Name

Acc#

hypothetical protein PH1114

pir:C71052

C71052

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25901467_c3_54	114	2034	88	267		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
30272051_f3_24	115	2035	248	747	169	2.2e-11

Protein name

Locus Name

Acc#

probable morphological
differentiation-associated protein

pir:T36679

T36679

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3323802_f3_23	116	2036	286	861	232	2.3e-19

Protein name

permease protein

Locus Name

gp:CJAJ750

Acc#

AJ000750

Description

Campylobacter jejuni malF gene, partial.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35976510_f3_30	117	2037	89	270	343	4.0e-31

Protein name

Locus Name

pir:FEKRV

Acc#

S72167:S78

121:A00210

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36383542_f1_13	118	2038	107	321	96	5.9e-05

Protein name

KH type splicing regulatory protein

Locus Name

gp:HSKHSRP3

Acc#

AF093747

Description

Homo sapiens KH type splicing regulatory protein (KHSRP) gene, exon2 and partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3923288_c1_39	119	2039	343	1032	254	1.1e-21

Protein name

probable regulatory protein (pfoS/R)

Locus Name

pir:E71373

Acc#

E71373

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3938393_c3_64	120	2040	218	657	726	1.0e-71

Protein name

uracil phosphoribosyltransferase, upp

Locus Name

pir:A65026

Acc#

A65026:S23

412

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4064638_f1_3	121	2041	371	1116	152	4.7e-08

Protein name

Locus Name

Acc#

sp:Y131_HAEIN

P43951

Description

HYPOTHETICAL PROTEIN HI0131 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4101568_f3_29	122	2042	263	792	512	4.9e-49

Protein name

Locus Name

Acc#

sp:FRP_VIBHA

Q56691

Description

(NADPH-FMN OXIDOREDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
682641_c1_33	123	2043	86	261	100	2.2e-05

Protein name

Locus Name

Acc#

hypothetical protein PH0217

pir:G71244

G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10790_f3_68	124	2044	731	2196	594	9.0e-86

Protein name

Locus Name

Acc#

sp:PRIM_HAEIN

Q08346

Description

DNA PRIMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
119012_c3_118	125	2045	438	1317	1830	1.1e-188

Protein name

Locus Name

Acc#

sp:YJCD_HAEIN

P44530

Description

HYPOTHETICAL PROTEIN HI0125

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12214386_c3_117	126	2046	125	378		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12540957_c3_121	127	2047	280	843	227	7.7e-19

Protein name

Locus Name

Acc#

probable yfiH protein

pir:A70579

A70579

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
12593961_f2_35	128	2048	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19532813_f3_73	129	2049	134	405	252	1.7e-21

Protein name

Locus Name

Acc#

RpST protein

gp:VCNHAR

AJ002395

Description

Vibrio cholerae nhaR, hlyU, mviN, and rpST genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
209375_c1_95	130	2050	750	2250	1867	1.3e-192

Protein name

Locus Name

Acc#

sp:CLPA_ECOLI

P15716:P77
686

Description

ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21641077_f2_49	131	2051	199	600	132	4.3e-08

Protein name

hypothetical protein

Locus Name

sp:SYCSLLE

Acc#

D64003:AB0
01339

Description

Synechocystis sp. PCC6803 complete genome, 22/27, 2755703-2868766.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22143827_c1_89	132	2052	250	753	246	7.5e-21

Protein name

Locus Name

sp:YIV8_YEAST

Acc#

P40582

Description

HYPOTHETICAL 26.8 KD PROTEIN IN HYR1 3'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22453453_c2_104	133	2053	426	1281	492	6.4e-47

Protein name

carboxyl-terminal proteinase

Locus Name

pir:F70369

Acc#

F70369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22831262_c1_94	134	2054	128	387	185	2.2e-14

Protein name

Locus Name

sp:YLJA_ECOLI

Acc#

P75832

Description

12.2 KD PROTEIN IN CSPD-CLPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23632215_f2_59	135	2055	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23645875_c1_84	136	2056	605	1818	723	2.1e-71

Protein name

Locus Name

Acc#

sp:CYDD_ECOLI

Description

P29018:Q47

656:P77275

TRANSPORT ATP-BINDING PROTEIN CYDD

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23875303_c2_109	137	2057	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24236642_c1_91	138	2058	350	1053	695	2.0e-68

Protein name

Locus Name

Acc#

sp:RLUD_ECOLI

Description

P33643:P77

003

(PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24317757_f3_67	139	2059	368	1107	352	4.4e-32

Protein name

Locus Name

Acc#

sp:YPIY_PSEAE

P33641

Description

HYPOTHETICAL 38.5 KD LIPOPROTEIN IN PILS 5' REGION PRECURSOR (ORFY)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24318805_f2_60	140	2060	205	618	229	4.8e-19

Protein name

Locus Name

Acc#

hypothetical protein

sp:ASA224767

AJ224767

Description

Acinetobacter sp. ADP1 lon gene and ORFs.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24417012_f2_52	141	2061	232	699	101	0.011

Protein name

LpsB

Locus Name

gp:AF193023

Acc#

AF193023

Description

Sinorhizobium meliloti GreA (greA), LpsB (lpsB), LpsE (lpsE), LpsD(lpsD), LpsC (lpsC), and Lrp (lrp) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24650062_c3_119	142	2062	234	705	148	3.1e-09

Protein name

hypothetical protein C33F10.3

Locus Name

pir:T15745

Acc#

T15745

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2468950_c3_123	143	2063	67	204	123	1.4e-06

Protein name

Locus Name

sp:COPA_HELFE

Acc#

032619

Description

COPPER-TRANSPORTING ATPASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25391941_c2_116	144	2064	298	897		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
261635_f1_16	145	2065	217	654	603	1.1e-58

Protein name

response regulator GacA

Locus Name

gp:AF115381

Acc#

AF115381

Description

Pseudomonas aureofaciens 30-84 response regulator GacA (gacA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31431512_f1_22	146	2066	182	549	295	4.8e-26

Protein name bacterioferritin comigratory protein Locus Name pir:F71971 Acc# F71971

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31832188_c2_114	147	2067	440	1323	1025	2.1e-103

Protein name Locus Name sp:Y290_HAEIN Acc# P77868

Description

PROBABLE CATION-TRANSPORTING ATPASE HI0290,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33845302_c2_115	148	2068	288	867	653	5.6e-64

Protein name Locus Name sp:Y290_HAEIN Acc# P77868

Description

PROBABLE CATION-TRANSPORTING ATPASE HI0290,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35974750_f2_38	149	2069	261	786	603	1.1e-58

Protein name Locus Name sp:YBGI_HAEIN Acc# Q57354:005008

Description

HYPOTHETICAL PROTEIN HI0105

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4806512_c2_96	150	2070	463	1392	1501	7.7e-154

Protein name hypothetical protein 7 Locus Name pir:T00129 Acc# T00129

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5109843_c2_99	151	2071	579	1740	291	4.3e-45

Protein name

Locus Name

Acc#

sp:CYDC_ECOLI

P23886

Description

TRANSPORT ATP-BINDING PROTEIN CYDC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6718_c2_103	152	2072	531	1596	1457	3.5e-149

Protein name

Locus Name

Acc#

sp:PMGI_ECOLI

P37689

Description

(EC 5.4.2.1) (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6837753_f1_23	153	2073	224	675	147	3.2e-08

Protein name

Locus Name

Acc#

capm protein (capMI) RP344

pir:B71691

B71691

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
789811_c1_88	154	2074	892	2679	2203	2.3e-256

Protein name

Locus Name

Acc#

sp:GYRA_ECOLI

P09097

Description

DNA GYRASE SUBUNIT A,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
986638_c3_5	155	2075	262	789	1149	1.5e-116

Protein name

Locus Name

Acc#

multidrug transporter homolog

pir:G69005

G69005

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12985037_c2_42	156	2076	158	477	354	1.9e-31

Protein name

Locus Name

Acc#

sp:PILQ_PSEAE

P34750

Description

FIMBRIAL ASSEMBLY PROTEIN PILQ PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14301467_c3_49	157	2077	231	696	316	2.9e-28

Protein name

Locus Name

Acc#

carbonic anhydrase

pir:D75298

D75298

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1557_c1_31	158	2078	501	1506	1393	2.1e-142

Protein name

Locus Name

Acc#

sp:YLEA_HAEIN

Q57163

Description

HYPOTHETICAL PROTEIN HI0019

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19615687_f1_6	159	2079	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23445308_f2_18	160	2080	224	672		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23859562_c1_32	161	2081	233	702	140	1.7e-09

Protein name

pilus expression protein

Locus Name

gp:PSEPONA

Acc#

L28837

Description

Pseudomonas syringae penicillin binding protein (ponA), membraneproteins (pilN, pilO), pilus expression proteins (pilM, pilP)genes, complete cds and pilus expression protein (pilQ) gene,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24040911_c1_33	162	2082	327	984	220	6.3e-30

Protein name

Locus Name

sp:PILQ_PSEAE

Acc#

P34750

Description

FIMBRIAL ASSEMBLY PROTEIN PILQ PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34510950_c2_39	163	2083	645	1938	201	4.9e-15

Protein name

membrane protein

Locus Name

gp:PSEPONA

Acc#

L28837

Description

Pseudomonas syringae penicillin binding protein (ponA), membraneproteins (pilN, pilO), pilus expression proteins (pilM, pilP)genes, complete cds and pilus expression protein (pilQ) gene,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34589061_c1_36	164	2084	183	552	365	1.8e-33

Protein name

lactoylglutathione lyase, :glyoxalase I

Locus Name

pir:A46714

Acc#

A46714:A46
623

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4304693_c1_34	165	2085	375	1128	883	2.4e-88

Protein name

Locus Name

Acc#

sp:AROB_NEIGO

050468

Description

3-DEHYDROQUINATE SYNTHASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4877328_c1_35	166	2086	318	957		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7042153_c2_43	167	2087	231	696	452	1.1e-42

Protein name

Locus Name

Acc#

sp:AROK_HAEIN

P43880

Description

SHIKIMATE KINASE, (SK)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7083457_c3_46	168	2088	216	651	154	4.2e-11

Protein name

Locus Name

Acc#

fimbrial assembly protein pilO

pir:S77728

S77728

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23703142_c1_3	169	2089	300	900	635	4.5e-62

Protein name

Locus Name

Acc#

sp:YJEK_ECOLI

P39280

Description

HYPOTHETICAL 38.7 KD PROTEIN IN MOPA-EFP INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34119052_f1_1	170	2090	204	612	663	4.9e-65

Protein name

translation elongation factor EF-P

Locus Name

pir:S34443

Acc#

S34443:S56

375:A65225

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32712915_c2_17	171	2091	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33984701_f3_10	172	2092	579	1740	1233	1.9e-125

Protein name

Locus Name

Acc#

sp:PMSR_NEIGO

P14930

Description

PEPTIDE METHIONINE SULFOXIDE REDUCTASE (PEPTIDE MET(O) REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36131500_c3_21	173	2093	308	927	655	3.4e-64

Protein name

Locus Name

Acc#

sp:HTPX_ECOLI

P23894

Description

PROBABLE PROTEASE HTPX, (HEAT SHOCK PROTEIN HTPX)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907578_c1_15	174	2094	299	900	572	2.1e-55

Protein name

Locus Name

Acc#

sp:DHPS_ECOLI

P26282:P78

110

Description

PYROPHOSPHORYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4100312_f3_13	175	2095	106	321		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
48828062_c2_16	176	2096	115	348	223	1.2e-16

Protein name Locus Name Acc#

probable transglycosylase

pir:T12796

T12796:A69
911

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
831318_f2_7	177	2097	472	1419	1225	1.4e-124

Protein name Locus Name Acc#

sp:HFLX_ECOLI

P25519

Description

GTP-BINDING PROTEIN HFLX

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
870250_f2_6	178	2098	255	768	394	1.6e-36

Protein name Locus Name Acc#

hypothetical protein in endA-gshB intergenic
region

pir:A65080

A65080

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10548386_f2_19	179	2099	647	1944		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10626558_c2_94	180	2100	182	549	73	0.039

Protein name

Locus Name

Acc#

sp:TEGP_HSV11

P06481

Description

TEGUMENT PHOSPHOPROTEIN US9 (10 KD PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1178127_f1_10	181	2101	445	1338	1319	1.5e-134

Protein name

Locus Name

Acc#

sp:SYS_HAEIN

P43833

Description

SERYL-TRNA SYNTHETASE, (SERINE--TRNA LIGASE) (SERRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12109686_c1_63	182	2102	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12892086_f2_26	183	2103	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1369428_c2_97	184	2104	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13710925_f3_46	185	2105	148	447	652	7.1e-64

Protein name

Locus Name

Acc#

sp:MT1C_MORBO

P34721

Description

METHYLTRANSFERASE MBOI C) (M.MBOI C)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1412642_c1_65	186	2106	147	444	88	0.00042

Protein name

Locus Name

Acc#

sp:YRK1_BACSU

P54436

Description

HYPOTHETICAL 8.2 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14250312_c2_100	187	2107	246	741		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
1433466_c2_111	188	2108	85	258	141	9.6e-09

Protein name

Locus Name

Acc#

sp:MVIN_ECOLI

P75932

Description

VIRULENCE FACTOR MVIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14875390_f3_51	189	2109	134	405	302	1.0e-26

Protein name

Locus Name

Acc#

sp:YAEI_ECOLI

P37764

Description

HYPOTHETICAL 49.1 KD PROTEIN IN CDSA-HLPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15020887_c1_83	190	2110	189	570		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15885450_c3_142	191	2111	342	1029	624	6.6e-61

Protein name

Locus Name

Acc#

sp:MVIN_HAEIN

P44958

Description

VIRULENCE FACTOR MVIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
166043_f1_8	192	2112	259	780	416	7.3e-39

Protein name

Locus Name

Acc#

cytochrome c maturation protein B

gp:AF044582

AF044582

Description

Shewanella putrefaciens NrfG homolog gene, partial cds; and mono-heme c-type cytochrome ScyA (scyA), cytochrome c maturation protein A (ccmA), cytochrome c maturation protein B (ccmB), cytochrome c maturation protein C (ccmC), cytochrome c maturation protein D (ccmD), and cytochrome c maturation protein E (ccmE) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17069628_f1_4	193	2113	116	351		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
187703_f2_21	194	2114	113	342	90	0.00026

Protein name

Locus Name

Acc#

sp:Y4AR_RHISN

P55365

Description

HYPOTHETICAL 12.1 KD PROTEIN Y4AR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22462757_c1_67	195	2115	67	204	89	0.00033

Protein name

hypothetical protein SC6E10.02

Locus Name

pir:T35489

Acc#

T35489

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23470003_c1_81	196	2116	155	468	346	2.3e-31

Protein name

Locus Name

sp:MVIN_ECOLI

Acc#

P75932

Description

VIRULENCE FACTOR MVIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23914017_c2_104	197	2117	88	267	134	5.5e-09

Protein name

hypothetical protein ydaT

Locus Name

pir:C69770

Acc#

C69770

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24219792_f2_34	198	2118	296	891	440	2.1e-41

Protein name

Locus Name

sp:CDSA_PSEAE

Acc#

Q59640

Description

SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24244033_c1_70	199	2119	302	909	620	1.8e-60

Protein name

Locus Name

sp:YGLA_SYNP2

Acc#

P28606

Description

HYPOTHETICAL 34.1 KD PROTEIN IN GLNA 3'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24252302_c2_106	200	2120	493	1482	1229	5.1e-125

Protein name

2-oxoglutarate/malate translocator homolog
yfls

Locus Name

pir:F69811

Acc#

F69811

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24330005_c3_122	201	2121	314	945	413	1.5e-38

Protein name

Locus Name

gp:AB017194

Acc#

AB017194

Description

Plectonema boryanum ORF270, proline iminopeptidase, ferredoxin and amidase
enhancer genes, complete and partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24650962_f3_45	202	2122	261	786	806	3.4e-80

Protein name

Locus Name

sp:T2D1_STRPN

Acc#

P09356

Description

(R.DPNI)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24735875_f2_16	203	2123	73	222	54	0.017

Protein name

Locus Name

sp:YMT0_YEAST

Acc#

Q04210

Description

HYPOTHETICAL 19.2 KD PROTEIN IN SUB1-ARGR1 INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25391007_c2_110	204	2124	216	651	443	1.0e-41

Protein name

N-acetyl-anhydromuramyl-L-alanine amidase

Locus Name

gp:AF082575

Acc#

AF082575

Description

Pseudomonas aeruginosa N-acetyl-anhydromuramyl-L-alanine amidase (ampD) and
transmembrane protein AmpE (ampE) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25662782_f2_24	205	2125	258	777	288	2.7e-25

Protein name

Locus Name

Acc#

sp:CCMA_RHOCA

P29959

Description

PROTEIN HELA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
289052_c1_66	206	2126	154	465	220	4.3e-18

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:B75344

B75344

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29301457_f3_44	207	2127	93	282		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29507800_c2_95	208	2128	397	1194	883	2.4e-88

Protein name

Locus Name

Acc#

sp:RP32_PSEAE

P42378

Description

RNA POLYMERASE SIGMA-32 FACTOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34569707_c3_131	209	2129	95	288	74	0.023

Protein name

Locus Name

Acc#

F22C12.13

gp:AC007764

AC007764

Description

Genomic sequence for Arabidopsis thaliana BAC F22C12 from chromosome I, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36335200_f1_13	210	2130	347	1044	506	2.1e-48

Protein name

Locus Name

Acc#

sp:YAEI_ECOLI

P37764

Description

HYPOTHETICAL 49.1 KD PROTEIN IN CDSA-HLPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36520625_f2_31	211	2131	256	771	723	2.1e-71

Protein name

Locus Name

Acc#

UMP kinase

gp:AB010087

AB010087

Description

Pseudomonas aeruginosa rpsB, tsf, pyrH, frr genes for ribosomalprotein S2, elongation factor Ts, UMP kinase, ribosome recyclingfactor, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907818_f2_32	212	2132	187	564	614	7.6e-60

Protein name

Locus Name

Acc#

ribosome recycling factor

gp:AB010087

AB010087

Description

Pseudomonas aeruginosa rpsB, tsf, pyrH, frr genes for ribosomalprotein S2, elongation factor Ts, UMP kinase, ribosome recyclingfactor, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
391068_f2_33	213	2133	272	819	534	2.3e-51

Protein name

Locus Name

Acc#

sp:UPPS_ECOLI

Q47675:P75
668

Description

(DI-TRANS-POLY-CIS-DECAPRENYLCISTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3915930_f3_50	214	2134	204	615	592	1.6e-57

Protein name

Locus Name

Acc#

sp:TKT1_ECOLI

P27302

Description

TRANSKETOLASE 1, (TK 1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3947932_f3_41	215	2135	299	900	125	2.0e-05

Protein name

Locus Name

Acc#

sp:YEEZ_ECOLI

P76370

Description

HYPOTHETICAL 29.7 KD PROTEIN IN SBCB-HISL INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4110687_f2_30	216	2136	497	1494	1775	7.1e-183

Protein name

Locus Name

Acc#

sp:TKT1_ECOLI

P27302

Description

TRANSKETOLASE 1, (TK 1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4345300_f2_20	217	2137	989	2970	2958	0.0

Protein name

Locus Name

Acc#

sp:SYV_HAEIN

P43834

Description

VALYL-TRNA SYNTHETASE, (VALINE--TRNA LIGASE) (VALRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4495268_c1_84	218	2138	110	333	512	4.9e-49

Protein name

Locus Name

Acc#

ferredoxin [3Fe-4S

pir:FEAV

A29936:A00
218

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4693768_f1_11	219	2139	435	1308	854	2.8e-85

Protein name

Locus Name

Acc#

sp:DXR_ECOLI

P45568:P77
209

Description

REDUCTOISOMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4772325_c1_69	220	2140	93	282	77	0.0071

Protein name cytochrome b Locus Name gp:ASA228475 Acc# AJ228475

Description

Andricus solitarius cytb gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5109626_f1_6	221	2141	81	246	355	2.1e-32

Protein name Locus Name sp:MT1A_MORBO Acc# P34720

Description

METHYLTRANSFERASE MBOI A) (M.MBOI A)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5350281_c3_139	222	2142	76	231		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6823912_f3_37	223	2143	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
103187_f2_5	224	2144	98	297		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16917_f2_4	225	2145	164	495	307	2.6e-27

Protein name

Locus Name

Acc#

sp:CYST_ECOLI

P16701

Description

SULFATE TRANSPORT SYSTEM PERMEASE PROTEIN CYST

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20163930_c1_9	226	2146	271	813	502	5.6e-48

Protein name

Locus Name

Acc#

sp:RHLB_HAEIN

P44922

Description

ATP-DEPENDENT RNA HELICASE RHLB HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24257755_c1_8	227	2147	155	468		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16594167_f1_5	228	2148	510	1533		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22897255_f2_6	229	2149	269	810	305	4.2e-27

Protein name

Locus Name

Acc#

putative acyltransferase

gp:SCM10

AL133469

Description

Streptomyces coelicolor cosmid M10.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24485937_f3_13	230	2150	62	189	147	1.7e-09

Protein name

glutamate dehydrogenase

Locus Name

gp:UAN010746

Acc#

AJ010746

Description

Antarctic bacterium TAD1, dhe gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2501562_f3_9	231	2151	288	867	547	9.5e-53

Protein name

Locus Name

sp:FTSH_ECOLI

Acc#

P28691

Description

CELL DIVISION PROTEIN FTSH,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25415636_f1_4	232	2152	679	2040	1148	7.4e-181

Protein name

Locus Name

sp:HTPG_ECOLI

Acc#

P10413

Description

PROTEIN C62.5)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26366686_c2_24	233	2153	791	2376	1520	7.5e-156

Protein name

penicillin-binding protein 1A

Locus Name

gp:PAU73780

Acc#

U73780

Description

Pseudomonas aeruginosa penicillin-binding protein 1A (ponA) gene, complete cds, and malic enzyme gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12304661_f2_18	234	2154	584	1755	763	1.2e-75

Protein name

Locus Name

sp:RECN_ECOLI

Acc#

P05824:P76
602

Description

DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16578133_c3_57	235	2155	65	198	74	0.013

Protein name

Locus Name

Acc#

sp:PSBR_TOBAC

Q40519

Description

PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR (PII10)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19564510_f2_17	236	2156	194	585	444	7.8e-42

Protein name

Locus Name

Acc#

N-formylmethionylaminoacyl-tRNA deformylase,

pir:S23107

S23107:S41
694:A49696
:B65121

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23554638_f3_29	237	2157	285	858	531	4.7e-51

Protein name

Locus Name

Acc#

beta-ketoacyl-acyl carrier protein synthase II

gp:AF188707

AF188707

Description

Photobacterium profundum acyl carrier protein (acpP) gene, partialcds; beta-ketoacyl-acyl carrier protein synthase II (fabF) gene, complete cds; and aminodeoxychorismate lyase (pabC) gene, partialcds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23912502_f1_9	238	2158	90	273	200	5.6e-16

Protein name

Locus Name

Acc#

sp:YHHP_ECOLI

P37618

Description

HYPOTHETICAL 9.1 KD PROTEIN IN FTSY-NIKA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23985753_f3_27	239	2159	167	504	273	1.0e-23

Protein name

Locus Name

Acc#

gp:ECU28377

U28377

Description

Escherichia coli K-12 genome; approximately 65 to 68 minutes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24302263_f1_6	240	2160	193	582	340	8.2e-31

Protein name Locus Name Acc#
hypothetical protein b2948 pir:C65080 C65080

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24353458_f2_20	241	2161	308	927	671	6.9e-66

Protein name Locus Name Acc#
site-specific recombinase gp:AF033497 AF033497

Description

Proteus mirabilis site-specific recombinase (xerD) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642562_f2_13	242	2162	102	309		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3007832_f2_19	243	2163	169	510		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36205013_f3_23	244	2164	361	1086	291	1.3e-25

Protein name Locus Name Acc#
hypothetical protein pir:G75388 G75388

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3953593_c1_39	245	2165	211	636	386	1.1e-35

Protein name

imidazoleglycerol-phosphate synthase

Locus Name

pir:D69070

Acc#

D69070

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4883425_f1_2	246	2166	206	621	234	1.4e-19

Protein name

Locus Name

sp:YQIA_ECOLI

Acc#

P36653

Description

HYPOTHETICAL 21.6 KD PROTEIN IN PARE-ICC INTERGENIC REGION (F193)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6506_f1_3	247	2167	637	1914	2041	4.6e-211

Protein name

topoisomerase IV subunit

Locus Name

gp:AB003429

Acc#

AB003429

Description

Pseudomonas aeruginosa DNA for topoisomerase IV subunit, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
805180_c1_38	248	2168	222	669	554	1.7e-53

Protein name

Locus Name

sp:HIS7_PEA

Acc#

Q43072

Description

IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE, (IGPD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
823381_f3_24	249	2169	134	405		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
862761_c1_43	250	2170	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12281888_c1_40	251	2171	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1367177_f2_15	252	2172	304	915	674	3.3e-66

Protein name

Locus Name

Acc#

sp:GALU_ECOLI

P25520

Description

URIDYLYLTRANSFERASE) (URIDINE DIPHOSPHOGLUCOSE PYROPHOSPHORYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14463877_f3_23	253	2173	330	993	273	1.0e-23

Protein name

Locus Name

Acc#

sp:YJGQ_ECOLI

P39341

Description

HYPOTHETICAL 39.8 KD PROTEIN IN PEPA-GNTV INTERGENIC REGION (O361)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
156515_f2_20	254	2174	178	537		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16040927_c2_50	255	2175	112	339		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16610183_c2_54	256	2176	310	933	569	4.4e-55

Protein name

Locus Name

Acc#

sp:TESB_ECOLI

P23911

Description

ACYL-COA THIOESTERASE II,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16819827_f1_6	257	2177	137	414		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19531885_c3_57	258	2178	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19538388_f2_14	259	2179	75	228	73	0.016

Protein name

Locus Name

Acc#

gp:SMI240618

AJ240618

Description

Streptococcus mitis xpt gene, strain 12261.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20942936_f3_27	260	2180	376	1131	1060	4.1e-107

Protein name

Locus Name

Acc#

sp:GALE_BACSU

P55180

Description

GALACTOSE 4-EPIMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21675051_f3_28	261	2181	321	966	447	3.8e-42

Protein name

Locus Name

Acc#

sp:YRFI_ECOLI

P45803

Description

HYPOTHETICAL 32.5 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23557930_c3_61	262	2182	619	1860	1768	3.9e-182

Protein name

Locus Name

Acc#

glucosamine synthase

gp:AF032884

AF032884:L
77909

Description

Thiobacillus ferrooxidans N-acetylglucosamine-1-phosphateuridylyltransferase (glmU) gene, partial cds; glucosamine synthase(glmS) and RecG (recG) genes, complete cds; and transposon Tn5468, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23634680_f2_18	263	2183	423	1272	383	2.3e-35

Protein name

Locus Name

Acc#

putative UDP-glucose dehydrogenase

gp:ALW243431

AJ243431

Description

Acinetobacter lwoffii wzc, wzb, wza, weeA, weeB, weeC, wzx, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24400250_f3_24	264	2184	860	2583	1162	6.4e-118

Protein name

Locus Name

Acc#

sp:PLSB_HAEIN

P44857

Description

GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE, (GPAT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24493801_f3_30	265	2185	375	1128	489	1.3e-46

Protein name

Locus Name

Acc#

FauI DNA methyltransferase

gp:AF029070

AF029070

Description

Flavobacterium aquatile FauI DNA methyltransferase (fauIM) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26797302_c2_55	266	2186	393	1182	515	2.3e-49

Protein name

Locus Name

Acc#

sp:YAIW_ECOLI

P77562

Description

HYPOTHETICAL 40.4 KD PROTEIN IN SBMA-DDLA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3317260_f1_5	267	2187	573	1722	1505	2.9e-154

Protein name

Locus Name

Acc#

putative phosphoglucose isomerase

gp:ALW243431

AJ243431

Description

Acinetobacter lwoffii wzc, wzb, wza, weeA, weeB, weeC, wxz, wzy, weeD, weeE, weeF, weeG, weeH, weeI, weeJ, weeK, galU, ugd, pgi, galE, pgm (partial) and mip (partial) genes (emulsan biosynthetic gene cluster), strain RAG-1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3938762_f2_22	268	2188	71	216	71	0.026

Protein name

Locus Name

Acc#

transcription regulator homolog yozG

pir:C69931

C69931

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6729635_c2_46	269	2189	171	516	94	0.0062

Protein name

hypothetical protein C45H4.14

Locus Name

pir:T32722

Acc#

T32722

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
976387_f2_19	270	2190	88	267	74	0.0025

Protein name

hypothetical protein T16L4.170

Locus Name

pir:T09929

Acc#

T09929

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10823462_c1_13	271	2191	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12376535_f2_5	272	2192	214	645	74	0.0011

Protein name

Locus Name

Acc#

gp:VCU39068

U39068

Description

Vibrio cholerae pathogenicity island, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22065635_f2_9	273	2193	521	1566	1440	2.2e-147

Protein name

sodium/proline symporter opuE:proline transporter opuE

Locus Name

pir:H69670

Acc#

H69670

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24228400_c1_20	274	2194	479	1440	1110	2.1e-112

Protein name

Locus Name

Acc#

sp:HEMN_ECOLI

Description

P32131:P76

772

(COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29328457_c1_14	275	2195	98	297	95	7.5e-05

Protein name

Locus Name

Acc#

sp:MINE_ECOLI

P18198

Description

CELL DIVISION TOPOLOGICAL SPECIFICITY FACTOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4880303_c1_19	276	2196	193	582	514	3.0e-49

Protein name

Locus Name

Acc#

sp:PTH_HAEIN

P44682

Description

PEPTIDYL-TRNA HYDROLASE, (PTH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6835875_f2_4	277	2197	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
900011_c3_28	278	2198	234	705	269	2.7e-23

Protein name

Locus Name

Acc#

probable ribosomal protein L25

pir:H71665

H71665

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9869006_f1_2	279	2199	72	219	271	1.7e-23

Protein name

30S subunit ribosomal protein S21

Locus Name

gp:AF014397

Acc#

AF014397

Description

Pseudomonas putida macromolecular synthesis operon: 30S subunit ribosomal protein S21 (rpsU), DNA primase (dnaG), and sigma-70 (rpoD) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11885875_c3_76	280	2200	455	1368	1218	7.5e-124

Protein name

Locus Name

sp:Y164_HAEIN

Acc#

P43955:P43
956

Description

HYPOTHETICAL PROTEIN HI0164/165

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12687781_c3_70	281	2201	174	525	512	4.9e-49

Protein name

Locus Name

sp:IF3_HAEIN

P43814

Description

TRANSLATION INITIATION FACTOR IF-3

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14093967_c1_49	282	2202	211	636	741	2.6e-73

Protein name

NqrE

Locus Name

gp:AF165980

Acc#

AF165980

Description

Vibrio harveyi Na⁺-translocating NADH-quinone oxidoreductase complex operon, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14540908_c3_77	283	2203	270	813	474	5.2e-45

Protein name

NqrC

Locus Name

gp:AF117331

Acc#

AF117331

Description

Vibrio cholerae N16961 Na⁺-translocating NADH-ubiquinoneoxidoreductase enzyme complex, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15865712_f2_21	284	2204	189	570	162	6.0e-12

Protein name

Locus Name

gp:ECOUW93

Acc#

U14003

Description

Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16460432_c2_65	285	2205	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22038177_f3_27	286	2206	557	1674	1801	1.2e-185

Protein name

putative efflux pump component MtrF

Locus Name

gp:AF176821

Acc#

AF176821

Description

Neisseria gonorrhoeae strain EU75 putative efflux pump componentMtrF (mtrF) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24423260_c1_42	287	2207	437	1314	121	2.5e-05

Protein name

pr2

Locus Name

gp:MHU19289

Acc#

U19289

Description

Mycoplasma hyopneumoniae J ATCC 27219 multidrug resistance proteinhomologs pr1 and pr2 genes, complete cds, and 23S rRNA gene,partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25392778_f1_1	288	2208	201	606	387	8.6e-36

Protein name

4-hydroxyphenylacetate 3-monooxygenase (EC

Locus Name

gp:D90737

Acc#

D90737:AB0

Description

01340

Escherichia coli genomic DNA. (22.8 - 23.1 min).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31268837_f3_28	289	2209	412	1239	1836	2.4e-189

Protein name

Locus Name

sp:CATA_HAEIN

Acc#

P44390

Description

CATALASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33223291_f2_19	290	2210	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33235937_c2_59	291	2211	782	2349	1415	1.0e-144

Protein name

Locus Name

sp:VACB_ECOLI

Acc#

P21499:P76

Description

800

VACB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33867132_f1_12	292	2212	225	678		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3399183_c2_61	293	2213	415	1248	1268	3.8e-129

Protein name

NqrB

Locus Name

gp:AF117331

Acc#

AF117331

Description

Vibrio cholerae N16961 Na⁺-translocating NADH-ubiquinoneoxidoreductase enzyme complex, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34000785_c3_73	294	2214	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34196052_c2_63	295	2215	416	1251	1650	1.2e-169

Protein name

NqrF

Locus Name

gp:AF117331

Acc#

AF117331

Description

Vibrio cholerae N16961 Na⁺-translocating NADH-ubiquinoneoxidoreductase enzyme complex, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939043_c2_58	296	2216	642	1929	2200	6.5e-228

Protein name

Locus Name

Acc#

sp:SYT_HAEIN

P43014

Description

(THRRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4720967_c2_62	297	2217	227	684	679	9.8e-67

Protein name

Locus Name

Acc#

sp:Y168_HAEIN

P43958:P43959

Description

HYPOTHETICAL PROTEIN HI0168/169

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
473137_c1_41	298	2218	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4801625_f2_20	299	2219	252	759	622	1.1e-60

Protein name

Locus Name

Acc#

sp:HIS4_RHOSH

P50936

Description

ISOMERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5882211_f2_14	300	2220	118	357	153	2.7e-10

Protein name

Locus Name

Acc#

hypothetical protein 1

pir:S47051

S47051

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
682641_c2_55	301	2221	86	261	100	2.2e-05

Protein name

Locus Name

Acc#

hypothetical protein PH0217

pir:G71244

G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14103377_f2_9	302	2222	166	501	434	9.0e-41

Protein name

Locus Name

Acc#

sp:MTGA_ACICA

O24849

Description

(EC 2.4.2.-) (MONOFUNCTIONAL TGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16973437_c3_30	303	2223	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19745308_f1_3	304	2224	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24261257_f3_14	305	2225	123	372	140	8.0e-09

Protein name

Locus Name

Acc#

sp:PNCB_SALTY

P22253

Description

NICOTINATE PHOSPHORIBOSYLTRANSFERASE, (NAPRTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25600925_f1_2	306	2226	91	276	98	9.9e-05

Protein name

Locus Name

Acc#

sp:MTGA_ACICA

O24849

Description

(EC 2.4.2.-) (MONOFUNCTIONAL TGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30659433_c2_21	307	2227	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3303178_f1_1	308	2228	179	540	430	2.4e-40

Protein name

solanesyl diphosphate synthase

Locus Name

gp:AB001997

Acc#

AB001997

Description

Rhodobacter capsulatus DNA for solanesyl diphosphate synthase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35182887_c2_23	309	2229	191	576	684	2.9e-67

Protein name

Locus Name

sp:IPYR_HAEIN

Acc#

P44529

Description

PHOSPHO-HYDROLASE) (PPASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36126655_f1_4	310	2230	374	1125	1283	9.7e-131

Protein name

Locus Name

sp:AROC_HAEIN

Acc#

P43875

Description

PHOSPHOLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6834702_f2_11	311	2231	162	489	371	4.3e-34

Protein name

Locus Name

sp:YCHJ_HAEIN

Acc#

P44609

Description

HYPOTHETICAL PROTEIN HI0277

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
882636_c1_15	312	2232	258	777	417	5.7e-39

Protein name

lipoate biosynthesis protein B

Locus Name

gp:AF147448

Acc#

AF147448

Description

Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 2 (pbpA), rod-shape-determining protein (rodA), membrane-bound lytic transglycosylase (mltB), rare lipoprotein A (rlpA), penicillin-binding protein 5 (dacA), and lipoate biosynthesis protein B (lipB) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
973756_c3_34	313	2233	138	417		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
975055_f2_10	314	2234	745	2238	2349	1.1e-243

Protein name Locus Name Acc#

polyphosphate kinase gp:ACRBDOXN 246863

Description

Acinetobacter sp. cysD, cobQ, sodM, lyss, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10673587_f1_4	315	2235	402	1209	1210	5.3e-123

Protein name Locus Name Acc#

sp:TYRB_ECOLI P04693

Description

AROMATIC-AMINO-ACID AMINOTRANSFERASE, (AROAT) (ARAT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14572162_f1_1	316	2236	260	783	586	7.0e-57

Protein name Locus Name Acc#

sp:YCIK_ECOLI P31808:P77
516

Description

(EC 1.-.-.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20126386_f2_8	317	2237	198	597	325	3.2e-29

Protein name Locus Name Acc#

sp:YTFL_ECOLI P39319

Description

HYPOTHETICAL 49.8 KD PROTEIN IN CYSQ-MSRA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2609375_c2_26	318	2238	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26808317_f2_6	319	2239	232	699	576	8.1e-56

Protein name

Locus Name

Acc#

sp:UBIG_ECOLI

Description

P17993:P76
924

METHYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34394050_f3_15	320	2240	308	927	889	5.5e-89

Protein name

Locus Name

Acc#

sp:YTFL_ECOLI

P39319

Description

HYPOTHETICAL 49.8 KD PROTEIN IN CYSQ-MSRA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3911568_f2_7	321	2241	233	702	267	4.5e-23

Protein name

Locus Name

Acc#

sp:GPHC_ALCEU

P40852

Description

PHOSPHOGLYCOLATE PHOSPHATASE, CHROMOSOMAL, (PGP)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4117193_c2_25	322	2242	506	1521	963	7.9e-97

Protein name

Locus Name

Acc#

leucine aminopeptidase

gp:PPU010261

AJ010261

Description

Pseudomonas putida pepA gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4144818_f3_16	323	2243	362	1089	766	5.9e-76

Protein name

probable ionicttransporter

Locus Name

pir:F70819

Acc#

F70819

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4976550_f1_3	324	2244	312	939	399	4.6e-37

Protein name

Locus Name

sp:YBHD_ECOLI

Acc#

P52696:P75
761

Description

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN MODC-BIOA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1441017_c1_38	325	2245	98	297	124	1.2e-07

Protein name

opacity protein opa51

Locus Name

pir:S36329

Acc#

S36329:S28
628

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14462827_c3_53	326	2246	89	270	292	1.0e-25

Protein name

ribosomal protein S15

Locus Name

pir:S38882

Acc#

S38882

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14494026_c2_50	327	2247	219	660	500	9.1e-48

Protein name

Locus Name

sp:HIS1_BACSU

Acc#

O34520

Description

ATP PHOSPHORIBOSYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14509682_c2_45	328	2248	165	498	230	3.7e-19

Protein name

Locus Name

Acc#

sp:VCU39068

U39068

Description

Vibrio cholerae pathogenicity island, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
157765_c2_48	329	2249	96	291	182	4.5e-14

Protein name

Locus Name

Acc#

sp:YRPM_ACICA

P33989

Description

HYPOTHETICAL 9.2 KD PROTEIN IN RPON-MURA INTERGENIC REGION (ORF3)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16510933_c2_52	330	2250	525	1578	545	1.6e-52

Protein name

Locus Name

Acc#

sp:FUMB_ECOLI

P14407:P78

139

Description

FUMARATE HYDRATASE CLASS I, ANAEROBIC, (FUMARASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23445931_c2_51	331	2251	454	1365	942	1.3e-94

Protein name

Locus Name

Acc#

histidinol dehydrogenase

pir:E70368

E70368

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23650253_c2_49	332	2252	421	1266	1337	1.8e-136

Protein name

Locus Name

Acc#

sp:MURA_ACICA

P33986

Description

TRANSFERASE) (EPT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2381950_c3_58	333	2253	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23867127_c1_41	334	2254	275	828	147	5.2e-10

Protein name

Locus Name

Acc#

sp:YRAP_ECOLI

P45467

Description

(O191)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24395637_c1_40	335	2255	149	450	143	6.2e-10

Protein name

Locus Name

Acc#

sp:YRAP_ECOLI

P45465

Description

HYPOTHETICAL 14.8 KD PROTEIN IN AGAI-MTR INTERGENIC REGION (O131)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34010260_f1_1	336	2256	119	360	204	2.1e-16

Protein name

Locus Name

Acc#

general stress protein homolog ykzA

pir:F69870

F69870

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5079188_f3_35	337	2257	163	492	461	1.2e-43

Protein name

Locus Name

Acc#

hypothetical protein

gp:ASA224767

AJ224767

Description

Acinetobacter sp. ADP1 lon gene and ORFs.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5330087_c3_61	338	2258	370	1113	922	1.7e-92

Protein name

Locus Name

Acc#

sp:HIS8_ACEXY

P45358

Description

PHOSPHATE TRANSAMINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
954837_c2_44	339	2259	699	2100	2198	1.1e-227

Protein name

Locus Name

Acc#

polyribonucleotide nucleotidyltransferase

gp:PPY18132

Y18132

Description

Pseudomonas putida rpsO and pnp genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
969392_f1_13	340	2260	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1070165_c3_42	341	2261	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10993750_f1_2	342	2262	137	414		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10355437_f2_5	353	2273	147	444	159	2.0e-11

Protein name

Locus Name

Acc#

sp:THID_HAEIN

P44697

Description

(HMP-P KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23912827_c3_10	354	2274	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35267912_c3_11	355	2275	306	921	483	5.8e-46

Protein name

Locus Name

Acc#

sp:PROC_HAEIN

P43869

Description

PYRROLINE-5-CARBOXYLATE REDUCTASE, (P5CR) (P5C REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4062840_c2_9	356	2276	191	576	206	1.3e-16

Protein name

Locus Name

Acc#

sp:YGGT_HAEIN

P44097

Description

HYPOTHETICAL PROTEIN HI1036

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10164063_c2_87	357	2277	242	729	425	8.1e-40

Protein name

Locus Name

Acc#

sp:YAEB_ECOLI

P28634

Description

HYPOTHETICAL 26.4 KD PROTEIN IN PROS-RCSF INTERGENIC REGION (ORF3)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14568812_c3_97	358	2278	426	1281	287	5.5e-37

Protein name

probable lipD protein

Locus Name

pir:G70634

Acc#

G70634

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14901512_c3_103	359	2279	156	471	210	4.9e-17

Protein name

Locus Name

sp:HIT_BACSU

Acc#

007513

Description

HIT PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
164813_f3_52	360	2280	431	1296	1416	7.8e-145

Protein name

Locus Name

gp:AB025342

Acc#

AB025342

Description

Moritella marina genes, complete cds, similar to eicosapentaenoic acid synthesis gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17068763_f1_16	361	2281	337	1014	1048	7.8e-106

Protein name

Locus Name

sp:HEM2_PSEAE

Acc#

Q59643

Description

SYNTHASE) (ALAD) (ALADH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23444400_c3_92	362	2282	336	1011	1151	9.4e-117

Protein name

Locus Name

sp:RUVB_ECOLI

Acc#

P08577

Description

HOLLIDAY JUNCTION DNA HELICASE RUVB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23526552_c2_83	363	2283	422	1269	316	2.9e-28

Protein name conserved hypothetical protein yueF Locus Name pir:G70007 Acc# G70007

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23595281_f1_17	364	2284	783	2352	2265	8.4e-235

Protein name hypothetical protein b2463 Locus Name pir:F65021 Acc# F65021

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23828428_f3_57	365	2285	272	819	250	1.6e-40

Protein name aldoketoreductase Locus Name gp:AF001865 Acc# AF001865

Description

Leishmania mexicana amazonensis aldoketoreductase (PTR-1) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24250012_c1_66	366	2286	576	1731	1104	9.0e-112

Protein name glycine betaine transporter BetL Locus Name gp:AF102174 Acc# AF102174

Description

Listeria monocytogenes glycine betaine transporter BetL (betL) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24313512_f2_37	367	2287	121	366		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24317157_f3_55	368	2288	179	540		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2517175_f1_18	369	2289	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29376681_f1_1	370	2290	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30360452_f1_6	371	2291	80	243		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30662517_c3_106	372	2292	479	1440	514	3.0e-49

Protein name

Locus Name

Acc#

sp:ACRE_ECOLI

P24180

Description

ACRIFLAVIN RESISTANCE PROTEIN E PRECURSOR (ENVC PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31423292_c2_80	373	2293	308	927	327	2.0e-29

Protein name

hypothetical protein Rv0241c

Locus Name

pir:E70938

Acc#

E70938

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31466_f3_54	374	2294	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34110436_f2_30	375	2295	116	351	83	0.030

Protein name

microfilarial sheath protein SHP3

Locus Name

gp:LSU54556

Acc#

U54556

Description

Litomosoides sigmodontis microfilarial sheath protein SHP3a (shp3a) and microfilarial sheath protein SHP3 (shp3) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4147193_f2_29	376	2296	635	1908	1651	3.4e-242

Protein name

dihydroxy-acid dehydratase,

Locus Name

pir:DWECDA

Acc#

A27310:D26

570:S48894

:S30669:F6

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4350088_c3_96	377	2297	458	1377	863	3.1e-86

Protein name

Locus Name

Acc#

gp:MLCB1883

AL022486

Description

Mycobacterium leprae cosmid B1883.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4381318_f3_56	378	2298	250	753	585	9.0e-57

Protein name

Locus Name

Acc#

sp:CCA_ECOLI

P06961

Description

(TRNA CCA-PYROPHOSPHORYLASE) (CCA-ADDING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4712537_c1_60	379	2299	117	354		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4769050_c2_79	380	2300	99	300	117	3.5e-07

Protein name

Locus Name

Acc#

hypothetical protein APE0395

pir:B72732

B72732

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5266540_f1_8	381	2301	219	660		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6250012_f1_7	382	2302	313	942	952	1.2e-95

Protein name

Locus Name

Acc#

ferredoxin--NADP+ reductase,

pir:A57432

A57432:A53
967

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6697266_c1_62	383	2303	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6817191_c2_89	384	2304	975	2925	2816	3.5e-293

Protein name

Locus Name

Acc#

sp:YHIV_ECOLI

P37637

Description

HYPOTHETICAL 111.5 KD PROTEIN IN HDED-GADA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781302_c3_98	385	2305	185	558	541	4.1e-52

Protein name

Locus Name

Acc#

sp:HPRT_ECOLI

P36766

Description

HYPOXANTHINE PHOSPHORIBOSYLTRANSFERASE, (HPRT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
100305_c3_168	386	2306	251	756	528	9.8e-51

Protein name

Locus Name

Acc#

sp:YHHW_ECOLI

P46852

Description

HYPOTHETICAL 26.3 KD PROTEIN IN GNTR-GGT INTERGENIC REGION (F231)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10604658_f2_36	387	2307	488	1467	705	1.7e-69

Protein name

Locus Name

Acc#

RdxB

gp:RSU67862

U67862

Description

Rhodobacter sphaeroides rdxB and rdxH genes, complete cds, and ccoP and rdxI genes, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12509836_f2_57	388	2308	137	414	178	1.2e-13

Description

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein SPAC869.06c	pir:T39117	T39117

Description

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
PiIT	gp:STAF000001	

Description

Salmonella typhi topoisomerase B (topB), single strand binding protein (ssb), Ytl2 homolog (ytl2) genes, complete cds; pil operon, complete sequence; Rci (rci) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13723751_c3_176	391	2311	423	1272	1357	1.4e-138

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
140_f1_11	392	2312	144	435		

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14650251_c1_125	393	2313	243	732	385	1.4e-35

Protein name

Locus Name

Acc#

sp:YGBP_HAEIN

005029

Description

HYPOTHETICAL PROTEIN HI0672

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
156261_f2_53	394	2314	158	477	522	4.3e-50

Protein name

Locus Name

Acc#

sp:RL13_HAEIN

P44387

Description

50S RIBOSOMAL PROTEIN L13

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15859456_f3_74	395	2315	96	291	105	6.6e-06

Protein name

Locus Name

Acc#

hypothetical protein PH0639

pir:H71108

H71108

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16803811_f1_13	396	2316	216	651	87	0.040

Protein name

Locus Name

Acc#

somatostatin sst2B receptor

gp:RNSST2B

X98234

Description

R.norvegicus mRNA for somatostatin receptor.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16853590_c3_164	397	2317	233	702	265	7.3e-23

Protein name

Locus Name

Acc#

sp:YEAZ_ECOLI

P76256:008

476:008477

Description

HYPOTHETICAL 25.2 KD PROTEIN IN FADD-PABE INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19563312_c2_137	398	2318	96	291	71	0.038

Protein name

Locus Name

Acc#

sp:YYAB_BACSU

P37523

Description

HYPOTHETICAL 17.0 KD PROTEIN IN SPO0J-GIDB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19632661_f3_91	399	2319	134	405		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
203577_c1_95	400	2320	751	2256	2566	1.1e-266

Protein name

Locus Name

Acc#

sp:CLPB_HAEIN

P44403

Description

CLPB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21988931_f3_88	401	2321	211	636	563	1.9e-54

Protein name

Locus Name

Acc#

sp:UCRI_CHRVI

O31214

Description

(RIESKE IRON-SULFUR PROTEIN) (RISP)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22066661_f2_40	402	2322	191	576	364	2.4e-33

Protein name

Locus Name

Acc#

sp:YAJQ_HAEIN

P44096

Description

HYPOTHETICAL PROTEIN HI1034

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23525307_c2_146	403	2323	213	642	554	3.5e-58

Protein name

cytochrome-c oxidase, type cbb3 chain fixO

Locus Name

pir:S77596

Acc#

S77596

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23720002_c2_140	404	2324	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23860681_f2_39	405	2325	455	1368	1917	6.4e-198

Protein name

Locus Name

Acc#

sp:ASSY_HAEIN

P44315

Description

LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23864180_f1_18	406	2326	271	816	254	1.1e-21

Protein name

Core

Locus Name

gp:AF130857

Acc#

AF130857

Description

Salmonella typhimurium cobalt resistance locus, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23947151_f1_19	407	2327	102	309	119	2.2e-07

Protein name

unknown

Locus Name

gp:AF147448

Acc#

AF147448

Description

Pseudomonas aeruginosa strain PAO1 penicillin-binding protein 2 (pbpA), rod-shape-determining protein (rodA), membrane-bound lytic transglycosylase (mltB), rare lipoprotein A (rlpA), penicillin-binding protein 5 (dacA), and lipote biosynthesis protein B (lipB) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24083208_f3_82	408	2328	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24271875_c1_122	409	2329	558	1677	1857	1.5e-191

Protein name

Locus Name

Acc#

sp:PYRG_HAEIN

P44341

Description

CTP SYNTHASE, (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24337827_f1_15	410	2330	355	1068	1038	8.9e-105

Protein name

Locus Name

Acc#

dihydroorotase,

pir:T10453

T10453

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24344138_f3_68	411	2331	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24417875_c1_124	412	2332	141	426	135	4.3e-09

Protein name

Locus Name

Acc#

sp:YGBQ_HAEIN

P44035

Description

HYPOTHETICAL PROTEIN HI0673

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24500286_c3_163	413	2333	519	1560	1458	2.6e-152

Protein name

Locus Name

Acc#

sp:SR54_ECOLI

P07019

Description

SIGNAL RECOGNITION PARTICLE PROTEIN (FIFTY-FOUR HOMOLOG) (P48)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648402_f1_22	414	2334	1298	3897	386	5.4e-59

Protein name

Locus Name

Acc#

probable exonuclease,

pir:T03465

T03465

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24844562_c3_167	415	2335	548	1647	1470	1.5e-150

Protein name

Locus Name

Acc#

probable pitB protein

pir:E70731

E70731

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29880042_f3_83	416	2336	485	1458	527	3.1e-61

Protein name

Locus Name

Acc#

sp:SBCE_ECOLI

P13457

Description

EXONUCLEASE SBCE

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3166026_f3_87	417	2337	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33204808_c1_101	418	2338	350	1053	231	2.8e-18

Protein name

hypothetical protein RP372

Locus Name

pir:E71694

Acc#

E71694

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3367635_f2_55	419	2339	421	1266	1355	2.3e-138

Protein name

Locus Name

sp:CYB_CHRVI

Acc#

031215

Description

CYTOCHROME B

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33707182_f1_27	420	2340	252	759	364	2.7e-46

Protein name

Locus Name

sp:CY1_CHRVI

Acc#

031216

Description

CYTOCHROME C1 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33875885_c3_157	421	2341	68	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34064681_c1_119	422	2342	87	264	71	0.026

Protein name

cb-type cytochrome c oxidase CcoQ subunit

Locus Name

gp:AB024290

Acc#

AB024290

Description

Magnetospirillum magnetotacticum ccoN, ccoO, ccoQ, ccoP gene forcb-type cytochrome c oxidase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34120251_c1_105	423	2343	322	969	647	2.4e-63

Protein name

Locus Name

Acc#

sp:UBIA_ECOLI

P26601

Description

POLYPRENYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36379680_c2_127	424	2344	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3906686_c3_155	425	2345	653	1962	2231	3.4e-231

Protein name

Locus Name

Acc#

sp:GIDA_PSEPU

P25756

Description

GLUCOSE INHIBITED DIVISION PROTEIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3932753_c2_149	426	2346	767	2304	235	1.3e-16

Protein name

Locus Name

Acc#

sp:REC2_HAEIN

P44408

Description

RECOMBINATION PROTEIN 2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3942318_f2_54	427	2347	131	396	507	1.7e-48

Protein name

Locus Name

Acc#

sp:RS9_HAESO

P31782

Description

30S RIBOSOMAL PROTEIN S9

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3947193_f2_56	428	2348	132	399	311	9.7e-28

Protein name

Locus Name

Acc#

sp:SSPB_HAEIN

P45206

Description

STRINGENT STARVATION PROTEIN B HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4119075_c1_103	429	2349	281	846	464	6.0e-44

Protein name

Locus Name

Acc#

sp:BACA_ECOLI

P31054:P39
203

Description

(EC 2.7.1.66)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4334463_c3_172	430	2350	169	510	78	2.8e-05

Protein name

Locus Name

Acc#

unknown

gp:AF083916

AF083916

Description

Rhizobium etli Fnr-type transcriptional regulator FnrNc (fnrNc) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4798193_c3_178	431	2351	358	1077	368	5.6e-48

Protein name

Locus Name

Acc#

cytochrome-c oxidase, fixP chain:cb-type
cytochrome-c oxidase 32K chain:cytochrome
b410:fixP protein

pir:D47468

D47468

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
500017_f3_73	432	2352	241	726	550	4.6e-53

Protein name

Locus Name

Acc#

sp:RNT_VIBPA

P46232

Description

RIBONUCLEASE T, (EXORIBONUCLEASE T) (RNASE T)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
520003_c1_126	433	2353	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5203453_c3_181	434	2354	445	1338	1467	3.1e-150

Protein name

Locus Name

Acc#

sp:ENO_ECOLI

P08324

Description

GLYCERATE HYDRO-LYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5281318_c3_180	435	2355	290	873	1037	1.1e-104

Protein name

Locus Name

Acc#

2-dehydro-3-deoxyphosphooctonate aldolase

gp:AF098791

AF098791

Description

Pseudomonas aeruginosa 2-dehydro-3-deoxyphosphooctonate aldolase (kdsA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
5901067_c1_104	436	2356	274	825	202	3.5e-16

Protein name

Locus Name

Acc#

sp:YHIQ_HAEIN

P44901

Description

HYPOTHETICAL PROTEIN HI0849

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7054650_c1_118	437	2357	62	189	53	0.015

Protein name

Locus Name

Acc#

ORF-D

gp:ECOI0KLS

D11109

Description

E. coli gene for 10K-L and 10K-S protein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
957705_c1_113	438	2358	335	1008	407	6.5e-38

Protein name putative regulatory protein Locus Name gp:AF087482 Acc# AF087482

Description

Pseudomonas aeruginosa clcC and ohbH genes, Lys-R type regulatory protein (clcR), chlorocatechol-1,2-dioxygenase (clcA), chloromuconate cycloisomerase (clcB), dienelactone hydrolase (clcD), maleylacetate reductase (clcE), transposase (tnpA), ATP-binding protein (tnpB), putative regulatory protein (ohbR), o-halobenzoate dioxygenase reductase (ohbA), o-halobenzoate dioxygenase alpha subunit (ohbB), o-halobenzoate dioxygenase beta subunit (ohbC),

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9960917_f3_90	439	2359	223	672	354	2.7e-32

Protein name Locus Name sp:SSPA_ECOLI Acc# P05838

Description

STRINGENT STARVATION PROTEIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10632090_f1_17	440	2360	506	1521	981	9.8e-99

Protein name Locus Name sp:NUON_ECOLI Acc#

Description P33608:P78281

OXIDOREDUCTASE CHAIN 14) (NUO14)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1069465_c1_85	441	2361	75	228		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10734830_c1_89	442	2362	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1385390_f3_54	443	2363	216	651	409	4.0e-38

Protein name

Locus Name

Acc#

sp:NUOJ_ECOLI

Description

P33605:P78
236

OXIDOREDUCTASE CHAIN 10) (NUO10)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13863425_f2_23	444	2364	276	831	480	1.2e-45

Protein name

Locus Name

Acc#

hypothetical protein RP682

pir:E71674

E71674

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14454827_f2_28	445	2365	211	636	561	3.1e-54

Protein name

Locus Name

Acc#

pyridoxamine 5-phosphate oxidase

pir:B75513

B75513

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14475702_c1_90	446	2366	259	780	91	0.00081

Protein name

Locus Name

Acc#

ORF8

gp:D78257

D78257

Description

Enterococcus faecalis plasmid pY117 genes for BacA, BacB, ORF3, ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14578202_f1_12	447	2367	182	549	763	1.2e-75

Protein name

Locus Name

Acc#

sp:NUOI_ECOLI

Description

P33604:P76
488:P78183

OXIDOREDUCTASE CHAIN 9) (NUO9)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15625443_c1_84	448	2368	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
175760_f3_46	449	2369	215	648	352	4.4e-32

Protein name

Locus Name

Acc#

NADH dehydrogenase chain A

gp:AF057063

AF057063

Description

Erwinia carotovora subsp. carotovora aspartate aminotransferase(aat) gene, partial cds; HexA (hexA), NADH dehydrogenase chain A(nuoA), and NADH dehydrogenase chain B (nuoB) genes, complete cds;and NADH dehydrogenase chain C (nuoC) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19806577_f2_27	450	2370	452	1359	1177	1.7e-119

Protein name

Locus Name

Acc#

sp:MRSA_HAEIN

P45164

Description

MRSA PROTEIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2110657_f1_3	451	2371	328	987	760	2.6e-75

Protein name

Locus Name

Acc#

sp:Y926_SYNY3

P72872

Description

HYPOTHETICAL 37.9 KD PROTEIN SLL0926

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22402252_f2_25	452	2372	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23683215_f2_38	453	2373	579	1740	1583	1.6e-162

Protein name

Locus Name

Acc#

sp:NUOM_ECOLI

Description

P31978:P78
248

OXIDOREDUCTASE CHAIN 13) (NUO13)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24225213_f3_50	454	2374	266	801	1183	3.8e-120

Protein name

Locus Name

Acc#

Tou2

gp:AF058689

AF058689

Description

Neisseria meningitidis strain Z2491, genomic sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24226502_c3_132	455	2375	270	813	888	7.0e-89

Protein name

Locus Name

Acc#

sp:Y572_HAEIN

P44758

Description

HYPOTHETICAL PROTEIN HI0572

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24391557_f1_10	456	2376	1046	3141	1655	8.6e-252

Protein name

Locus Name

Acc#

NADH dehydrogenase (ubiquinone), I chain
G:nuoK protein

pir:A65000

A65000:S65
638:S38316
:S37064

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642893_f1_15	457	2377	619	1860	1809	1.8e-186

Protein name

Locus Name

Acc#

sp:NUOL_ECOLI

Description

P33607:P78
254

OXIDOREDUCTASE CHAIN 12) (NUO12)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2507286_f2_22	458	2378	213	642	770	2.2e-76

Protein name

outer membrane protein B1

Locus Name

gp:AF045251

Acc#

AF045251

Description

Moraxella catarrhalis outer membrane protein B1 gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25392135_f2_26	459	2379	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25579763_f3_61	460	2380	281	846	374	2.3e-39

Protein name

Locus Name

Acc#

sp:FENR_ECOLI

Description

P28861:P11
007

(FLXR) (FLDR) (METHYL VIOLOGEN RESISTANCE PROTEIN A) (DA1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26228401_c2_105	461	2381	156	471	123	8.1e-08

Protein name

hypothetical protein APE1413

Locus Name

pir:D72619

Acc#

D72619

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29688176_f1_1	462	2382	70	213	304	4.8e-26

Protein name

transferrin-binding protein 2 precursor

Locus Name

gp:AF105251

Acc#

AF105251

Description

Moraxella catarrhalis transferrin-binding protein 2 precursor(ompB1) gene, partial cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
30082693_f3_51	463	2383	491	1476	1378	8.3e-141

Protein name

Description

Locus Name
sp:NUOF_ECOLI

Acc#
P31979:P78
239

OXIDOREDUCTASE CHAIN 6) (NUO6)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
30252036_c2_98	464	2384	63	192		

Protein name

Description

Locus Name

Acc#

NO-HIT

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
31283452_f1_11	465	2385	342	1029	1126	4.2e-114

Protein name

Description

Locus Name
sp:NUOH_ECOLI

Acc#
P33603:P78
307

OXIDOREDUCTASE CHAIN 8) (NUO8)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
3182067_c3_131	466	2386	516	1551	1966	4.1e-203

Protein name

Description

Locus Name
sp:SYR_HAEIN

Acc#
P43832

ARGINYL-TRNA SYNTHETASE, (ARGININE--TRNA LIGASE) (ARGRS)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
33723387_f1_6	467	2387	235	708	799	1.9e-79

Protein name

Description

Locus Name
sp:NUOB_ECOLI

Acc#
P33598:P78
090

OXIDOREDUCTASE CHAIN 2) (NUO2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33772186_f3_41	468	2388	416	1251	1601	1.9e-164

Protein name

transferrin binding protein B

Locus Name

gp:AF039313

Acc#

AF039313

Description

Moraxella catarrhalis strain LES-1 transferrin binding protein B(tbpB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34176950_f3_42	469	2389	548	1647	331	2.2e-29

Protein name

Locus Name

sp:Y170_METJA

Acc#

Q57634

Description

HYPOTHETICAL PROTEIN MJ0170

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34414552_f3_47	470	2390	584	1755	2190	7.5e-227

Protein name

NADH dehydrogenase (ubiquinone), I, chain C-D

Locus Name

pir:D65000

Acc#

D65000:S38
313:S38312
:S65634:S6

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35166075_f1_4	471	2391	294	885	315	3.7e-28

Protein name

periplasmic chaperone protein

Locus Name

gp:AF095845

Acc#

AF095845

Description

Pseudomonas syringae cell division/stress response protein (ftsK) and periplasmic chaperone protein (lola) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36144687_f3_49	472	2392	62	189	240	3.2e-20

Protein name

Locus Name

sp:NUOD_SALTY

Acc#

P33902

Description

OXIDOREDUCTASE CHAIN 4) (NUO4) (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3915693_c1_80	473	2393	416	1251	211	1.7e-14

Protein name

Locus Name

Acc#

gp:ECPMC7A

X57583

Description

E.coli Plasmid pMccC7 mcca,B,C,D,E,F genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4740902_c2_127	474	2394	313	942	114	0.00043

Protein name

Locus Name

Acc#

sp:PRXH_BPMD2

O64252

Description

PUTATIVE NON-HEME HALOPEROXIDASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4796875_f1_5	475	2395	78	237	144	4.8e-10

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:H75273

H75273

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5097886_f1_14	476	2396	145	438	320	1.1e-28

Protein name

Locus Name

Acc#

sp:NUOK_ECOLI

P33606:P76

487:P78182

Description

OXIDOREDUCTASE CHAIN 11) (NUO11)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7226452_f1_9	477	2397	174	525	470	1.4e-44

Protein name

Locus Name

Acc#

sp:NUOE_SALTY

P33903

Description

OXIDOREDUCTASE CHAIN 5) (NUO5)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10181576_f2_42	478	2398	101	306		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10751312_f1_7	479	2399	939	2820	710	2.9e-114

Protein name

Locus Name

Acc#

sp:YCBY_HAEIN

Description

P44524:P43
945

HYPOTHETICAL PROTEIN HI0116/115

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10975302_c1_93	480	2400	293	882	185	2.5e-13

Protein name

Locus Name

Acc#

probable D,D-carboxypeptidase

pir:B71353

B71353

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19587762_c1_77	481	2401	89	270		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19735877_f2_34	482	2402	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21491075_c3_127	483	2403	517	1554	309	1.4e-41

Protein name

CjaB protein

Locus Name

gp:CJE17971

Acc#

Y17971

Description

Campylobacter jejuni cjaB gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21520276_c3_136	484	2404	275	828		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21603403_c3_126	485	2405	543	1632	857	1.3e-85

Protein name

Locus Name

Acc#

sp:YMDC_ECOLI

P75919

Description

HYPOTHETICAL 55.9 KD PROTEIN IN CSGC-MDOG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21679677_f3_58	486	2406	476	1431	1649	1.6e-169

Protein name

Locus Name

Acc#

sp:GLNA_AZOVI

P22248

Description

GLUTAMINE SYNTHETASE, (GLUTAMATE--AMMONIA LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22306532_c3_134	487	2407	255	768	426	6.3e-40

Protein name

Locus Name

Acc#

sp:LPSA_PASHA

Q05770

Description

LPSA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22442010_f1_1	488	2408	354	1065	450	1.8e-42

Protein name unknown Locus Name gp:AF116284 Acc# AF116284

Description

Pseudomonas aeruginosa DnaJ-like protein gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2375337_f3_49	489	2409	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23944431_c2_116	490	2410	80	243	106	5.1e-06

Protein name Locus Name Acc#
hypothetical protein APE0029 pir:H72754 H72754

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23945931_f3_55	491	2411	346	1041	136	1.2e-06

Protein name Locus Name Acc#
hypothetical protein slr1166 pir:S75877 S75877

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23954511_f1_6	492	2412	811	2436	2745	1.2e-285

Protein name Locus Name Acc#
sp:PPSA_ECOLI P23538

Description

(PEP SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23989752_c1_84	493	2413	166	501	288	1.0e-42

Protein name

Locus Name

Acc#

sp:3DHQ_NEUCK

P05195

Description

DEHYDRATASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24306512_c2_99	494	2414	202	609	509	1.0e-48

Protein name

Locus Name

Acc#

sp:GCH1_OSTOS

O61573

Description

GTP CYCLOHYDROLASE I, (GTP-CH-I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24337752_f2_32	495	2415	378	1137	884	1.9e-88

Protein name

Locus Name

Acc#

sp:YDAO_ECOLI

P76055:Q47
558

Description

HYPOTHETICAL 35.6 KD PROTEIN IN DEPA-INTR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24646887_f1_16	496	2416	169	510		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24881717_f2_39	497	2417	107	324		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25595262_f3_68	498	2418	168	507		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26354750_f3_50	499	2419	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29332503_f3_66	500	2420	301	906	797	3.1e-79

Protein name Locus Name Acc#

enoyl-(acyl-carrier protein) reductase gp:AF104262 AF104262

Description

Pseudomonas aeruginosa enoyl-(acyl-carrier protein) reductase(fabI) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29335786_f3_46	501	2421	249	750	428	3.9e-40

Protein name Locus Name Acc#

unknown gp:AF116284 AF116284

Description

Pseudomonas aeruginosa DnaJ-like protein gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29382075_f1_4	502	2422	312	939	429	3.0e-40

Protein name Locus Name Acc#

probable membrane protein b1520 pir:C64906 C64906

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31425825_f1_22	503	2423	220	663	771	1.7e-76

Protein name

Locus Name

Acc#

sp:RPE_HAEIN

P44756

Description

EPIMERASE) (PPE) (R5P3E)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32177_c3_133	504	2424	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3316436_f1_19	505	2425	462	1389	331	7.4e-30

Protein name

Locus Name

Acc#

sp:VISC_ECOLI

P25535

Description

VISC PROTEIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33632828_f3_62	506	2426	249	750	559	5.1e-54

Protein name

Locus Name

Acc#

ribose-5-phosphate isomerase

gp:AF037440

AF037440

Description

Edwardsiella ictaluri D-3-phosphoglycerate dehydrogenase (serA) gene, partial cds; ribose-5-phosphate isomerase (rpiA), inhibitor of chromosome initiation (iciA), putative 26 kDa protein (yggE), putative 30.6 kDa protein (yggB), and fructose 1,6-bisphosphate aldolase (fda) genes, complete cds; and phosphoglycerate kinase (pgk) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33863431_f3_53	507	2427	430	1293	456	4.2e-43

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:F75546

F75546

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35163902_c2_109	508	2428	627	1884	960	8.9e-103

Protein name

Locus Name

Acc#

sp:MSBA_ECOLI

P27299

Description

PROBABLE TRANSPORT ATP-BINDING PROTEIN MSBA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35350061_c2_98	509	2429	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36128378_f3_67	510	2430	124	375		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3912568_c1_92	511	2431	525	1578	1470	1.5e-150

Protein name

Locus Name

Acc#

soluble pyridine nucleotide transhydrogenase

gp:AF159108

AF159108

Description

Azotobacter vinelandii soluble pyridine nucleotide transhydrogenase (sth) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4111008_f2_33	512	2432	94	285	240	3.2e-20

Protein name

Locus Name

Acc#

sp:CSPA_PSEAE

P95459

Description

MAJOR COLD SHOCK PROTEIN CSPA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4500892_c1_91	513	2433	291	876	599	2.9e-58

Protein name

Locus Name

Acc#

sp:YDIA_ECOLI

Description

P03822:P46

137:P76203

HYPOTHETICAL 31.2 KD PROTEIN IN PPSA-AROH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5132667_f1_12	514	2434	368	1107	124	6.4e-05

Protein name

Locus Name

Acc#

mannosyltransferase-like protein

gp:YPS251712

AJ251712

Description

Yersinia pseudotuberculosis serotype O:1b hemH gene (partial) and O-antigen gene cluster for ddhD gene, ddhA gene, ddhB gene, ddhC gene, prt gene, wbyH gene, wzx gene, wbyI gene, wbyJ gene, wzy gene, wbyK gene, gmd gene, fcl gene, manC gene, wbyL gene, manB gene and wzz gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5859762_c2_120	515	2435	115	348		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5894501_c1_82	516	2436	551	1656	564	1.5e-54

Protein name

Locus Name

Acc#

sp:Y653_HAEIN

P44029

Description

HYPOTHETICAL PROTEIN HI0653

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5993768_c2_122	517	2437	514	1542	305	4.6e-24

Protein name

Locus Name

Acc#

sp:OSTA_HAEIN

P44846

Description

ORGANIC SOLVENT TOLERANCE PROTEIN HOMOLOG PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33986343_f3_10	523	2443	699	2100	2411	2.9e-250

Protein name

oligopeptidpermease

Locus Name

gp:SPOPPDACA

Acc#

X89237

Description

S.pyogenes DNA for oppA, oppB, oppC, oppD, oppF, and dacA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4727338_f3_9	524	2444	325	978	1264	1.0e-128

Protein name

oligopeptidpermease

Locus Name

gp:SPOPPDACA

Acc#

X89237

Description

S.pyogenes DNA for oppA, oppB, oppC, oppD, oppF, and dacA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4788508_f3_11	525	2445	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6053212_f3_8	526	2446	340	1023	1398	6.3e-143

Protein name

oligopeptidpermease

Locus Name

gp:SPOPPDACA

Acc#

X89237

Description

S.pyogenes DNA for oppA, oppB, oppC, oppD, oppF, and dacA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12265658_c2_101	527	2447	221	666	753	1.4e-74

Protein name

Locus Name

Acc#

sp:DP3X_HAEIN

P43746

Description

DNA POLYMERASE III SUBUNIT GAMMA/TAU,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12501562_c2_109	528	2448	214	645	254	3.5e-21

Protein name

hemolysin-related protein

Locus Name

pir:F72326

Acc#

F72326

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12605253_c1_85	529	2449	967	2904	563	1.3e-65

Protein name

Locus Name

sp:MLTD_ECOLI

Acc#

P23931:P32
982:P77350

Description

(MUREIN HYDROLASE D) (REGULATORY PROTEIN DNIR)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12891082_f3_51	530	2450	237	714	234	1.4e-19

Protein name

Locus Name

sp:YBHD_ECOLI

Acc#

P52696:P75
761

Description

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN MODC-BIOA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13876010_f1_11	531	2451	135	408	156	7.0e-11

Protein name

Locus Name

sp:RBCR_CHRVI

Acc#

P25544

Description

RUBISCO OPERON TRANSCRIPTIONAL REGULATOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15870706_c1_68	532	2452	344	1035	1009	1.1e-101

Protein name

Locus Name

sp:LEU2_ECOLI

Acc#

P30127:P78
042

Description

(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
175062_c1_79	533	2453	219	660	740	3.4e-73

Protein name

Locus Name

Acc#

sp:HPPD_PSESP

P80064

Description

4-HYDROXYPHENYLPYRUVATE DIOXYGENASE, (4HPPD) (HPD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19769052_c1_74	534	2454	131	396	294	2.0e-25

Protein name

Locus Name

Acc#

sp:SYK_ACICA

Q43990

Description

LYSYL-TRNA SYNTHETASE, (LYSINE--TRNA LIGASE) (LYSRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20178438_c1_80	535	2455	173	522	629	1.9e-61

Protein name

Locus Name

Acc#

sp:HPPD_PSESP

P80064

Description

4-HYDROXYPHENYLPYRUVATE DIOXYGENASE, (4HPPD) (HPD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21729513_c3_129	536	2456	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21738306_f2_30	537	2457	100	303	185	4.9e-14

Protein name

Locus Name

Acc#

sp:SECF_HAEIN

P44590

Description

PROTEIN-EXPORT MEMBRANE PROTEIN SECF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22443750_c3_128	538	2458	201	606	166	8.1e-12

Protein name

Locus Name

Acc#

sp:YC54_SYNY3

P74078

Description

HYPOTHETICAL 38.3 KD PROTEIN SLL1254

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23572128_c1_92	539	2459	103	312	179	6.0e-13

Protein name

Locus Name

Acc#

sp:RADA_PSEAE

P96963

Description

DNA REPAIR PROTEIN RADA HOMOLOG (DNA REPAIR PROTEIN SMS HOMOLOG)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23614376_c3_119	540	2460	312	939	742	2.1e-73

Protein name

Locus Name

Acc#

sp:EX3_HAEIN

P44318

Description

EXODEOXYRIBONUCLEASE III, (EXONUCLEASE III) (EXO III)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23994182_f1_17	541	2461	171	516	175	2.5e-13

Protein name

Locus Name

Acc#

orf1

gp:PAU39558

U39558

Description

Pseudomonas aeruginosa orf1, TolQ (tolQ), TolR (tolR), TolA (tolA), and TolB (tolB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24276625_c3_122	542	2462	293	882	337	1.7e-30

Protein name

Locus Name

Acc#

sp:YGIP_ECOLI

P45463

Description

HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN BACA-TTDA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24406575_c1_69	543	2463	227	684	780	1.9e-77

Protein name

Locus Name

Acc#

sp:LEUD_AZQVI

P96196

Description

(ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415911_c3_115	544	2464	97	294	97	4.6e-05

Protein name

Locus Name

Acc#

outer membrane protein H.8 precursor

pir:S04157

S04157

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24417077_c3_121	545	2465	555	1668	229	9.9e-16

Protein name

Locus Name

Acc#

sp:DP3X_HAEIN

P43746

Description

DNA POLYMERASE III SUBUNIT GAMMA/TAU,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25584501_c2_110	546	2466	230	693		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30198405_c2_100	547	2467	417	1254	1913	1.7e-197

Protein name

Locus Name

Acc#

sp:SYK_ACICA

Q43990

Description

LYSYL-TRNA SYNTHETASE, (LYSINE--TRNA LIGASE) (LYSRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34406268_c1_70	548	2468	169	510		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3912568_c2_105	549	2469	467	1404	819	1.4e-81

Protein name

Locus Name

Acc#

sp:NHAC_BACFI

P27611

Description

NA(+)/H(+) ANTIPORTER

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3953377_c3_117	550	2470	218	657	534	3.1e-51

Protein name

Locus Name

Acc#

sp:LEU2_CANMA

Q00464

Description

ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3988813_f1_4	551	2471	628	1887	1391	3.5e-142

Protein name

Locus Name

Acc#

general protein secretion pathway subunit
SecD

gp:AF179925

AF179925

Description

Citrobacter freundii general protein secretion pathway subunit SecDgene,
complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4314068_c3_118	552	2472	359	1080	1356	1.8e-138

Protein name

Locus Name

Acc#

sp:LEU3_NEILA

P50180

Description

(IMDH) (3-IPM-DH) (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4335328_c2_98	553	2473	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4487638_f1_1	554	2474	613	1842	1886	1.2e-194

Protein name

Locus Name

Acc#

sp:PPCK_CHLLI

Q08262

Description

(PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4771925_c2_94	555	2475	207	624	331	7.4e-30

Protein name

Locus Name

Acc#

sp:RUVA_PSEAE

Q51425

Description

HOLLIDAY JUNCTION DNA HELICASE RUVA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4866427_f3_61	556	2476	289	870	247	5.9e-21

Protein name

Locus Name

Acc#

hypothetical protein

pir:S75235

S75235

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4881338_f1_5	557	2477	287	864	420	2.7e-39

Protein name

Locus Name

Acc#

sp:SECF_HAEIN

P44590

Description

PROTEIN-EXPORT MEMBRANE PROTEIN SECF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5084463_f2_28	558	2478	114	345	240	3.2e-20

Protein name

Locus Name

Acc#

sp:YAJC_ECOLI

P19677

Description

HYPOTHETICAL 11.9 KD PROTEIN IN TGT-SECD INTERGENIC REGION (ORF12)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5111588_c3_116	559	2479	348	1047	1466	3.9e-150

Protein name

Locus Name

Acc#

fructose-1,6-bisphosphate aldolase

gp:PST011927

AJ011927

Description

Pseudomonas stutzeri fda gene and gene encoding hypotheticalprotein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
978400_c1_83	560	2480	387	1164	503	4.4e-48

Protein name

Locus Name

Acc#

penicillin-binding protein 4

gp:AF156692

AF156692

Description

Neisseria gonorrhoeae penicillin-binding protein 4 (pbp4) gene,complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1053753_f3_63	561	2481	588	1767	801	1.2e-79

Protein name

Locus Name

Acc#

putative membrane protein

gp:AF150928

AF150928

Description

Acinetobacter sp. ADP1 BenP (benP) and AreR (areR) genes, completecds; are operon, complete sequence; SalD (salD), and Sale (sale)genes, complete cds; SalR (salR), SalA (salA), putative membraneprotein, putative 2-component regulatory protein, putativehistidine kinase of 2-component regulatory system, and carbonicanhydrase homolog genes, complete cds; and dihydropyrimidinasehomolog gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1058425_c2_108	562	2482	80	243	310	1.2e-27

Protein name

Locus Name

Acc#

ribosomal protein S18

pir:E64076

E64076

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1203450_f1_5	563	2483	530	1593	1297	3.2e-132

Protein name

Locus Name

Acc#

sp:YB2X_HAEIN

086233

Description

HYPOTHETICAL PROTEIN HI1126.1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12271926_c1_71	564	2484	143	432	197	1.2e-15

Protein name

Locus Name

Acc#

sp:YFFB_HAEIN

P44515

Description

HYPOTHETICAL PROTEIN HI0103

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15635930_f3_61	565	2485	373	1122	842	5.2e-84

Protein name

Locus Name

Acc#

sp:QUEA_ECOLI

P21516

Description

(QUEUOSINE BIOSYNTHESIS PROTEIN QUEA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16134657_f2_24	566	2486	367	1104	895	1.3e-89

Protein name

Locus Name

Acc#

sp:GCST_ECOLI

P27248

Description

PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
197211_c1_91	567	2487	240	723	304	5.4e-27

Protein name

Locus Name

Acc#

hypothetical protein

gp:ACRBDOXN

Z46863

Description

Acinetobacter sp. cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR, ppk, mtgA, ORF2 and ORF3 genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20890660_f3_56	568	2488	121	366		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20915682_f1_1	569	2489	142	429	162	6.0e-12

Protein name Locus Name Acc#

sp:YIBN_ECOLI P37688

Description

HYPOTHETICAL 15.6 KD PROTEIN IN SECB-TDH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21759656_f1_8	570	2490	591	1776	630	1.6e-103

Protein name Locus Name Acc#

Na(+):solute symporter (Ssf family) pir:E70480 E70480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22353380_f1_7	571	2491	89	270		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23438426_f2_26	572	2492	961	2886	2873	3.1e-299

Protein name Locus Name Acc#

sp:GCSP_ECOLI P33195

Description

DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23444531_f2_25	573	2493	138	417	411	2.5e-38

Protein name

glycine cleavage system protein
H:aminomethyl carrier protein:glycine
decarboxylase complex protein H

Locus Name

pir:A56623

Acc#

A56623:S36
833:B56689
:I41231:H6

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24391340_f3_47	574	2494	82	249		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24397200_f2_32	575	2495	410	1233	1330	1.0e-135

Protein name

Locus Name

Acc#

sp:TGT_HAEIN

P44594

Description

TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25400263_c3_117	576	2496	399	1200	725	1.3e-71

Protein name

Locus Name

Acc#

sp:YCAB_PSEFR

P72190

Description

HYPOTHETICAL 30.2 KD PROTEIN IN CAPB 3'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25562762_f2_18	577	2497	109	330	199	7.2e-16

Protein name

glutaredoxin 3 (grxC1) RP204

Locus Name

pir:F71731

Acc#

F71731

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25626452_c3_125	578	2498	106	321	129	1.9e-08

Protein name

Locus Name

Acc#

sp:YCGI_ECOLI

P76003

Description

HYPOTHETICAL 12.4 KD PROTEIN IN MINC-SHEA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
282550_c3_110	579	2499	316	951	127	2.3e-05

Protein name

Locus Name

Acc#

hypothetical protein

sp:SFR236923

AJ236923

Description

Shewanella frigidimarina ifcA gene and ORF2 (partial) and ORF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29314057_c1_90	580	2500	289	870	705	1.7e-69

Protein name

Locus Name

Acc#

probable ion transporter

pir:E75470

E75470

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29333458_f2_39	581	2501	143	432	196	2.7e-14

Protein name

Locus Name

Acc#

sp:SYL_SYNY3

P73274

Description

LEUCYL-TRNA SYNTHETASE, (LEUCINE--TRNA LIGASE) (LEURS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30100432_f3_66	582	2502	361	1086	128	2.3e-05

Protein name

Locus Name

Acc#

sp:HOLA_ECOLI

P28630

Description

DNA POLYMERASE III, DELTA SUBUNIT,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3298257_f1_16	583	2503	178	537		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35637_f2_30	584	2504	165	498	146	3.0e-10

Protein name

Locus Name

Acc#

unknown

gp:AF064527

AF064527

Description

Rhodocista centenaria PPH (pph) gene, complete cds; and unknowngenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907781_c3_126	585	2505	170	513		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3925443_c2_107	586	2506	136	411	369	6.9e-34

Protein name

Locus Name

Acc#

sp:RS6_ECOLI

P02358

Description

30S RIBOSOMAL PROTEIN S6

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4003558_f1_2	587	2507	157	474	508	1.3e-48

Protein name

Locus Name

Acc#

sp:DUT_ECOLI

P06968

Description

(DUTPASE) (DUTP PYROPHOSPHATASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4328443_f3_43	588	2508	151	456	393	2.0e-36

Protein name

Locus Name

Acc#

sp:SECB_ECOLI

P15040

Description

PROTEIN-EXPORT PROTEIN SECB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4860762_f3_64	589	2509	268	807		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4860943_c1_89	590	2510	185	558	199	7.2e-16

Protein name

Locus Name

Acc#

NADPH:quinone oxidoreductase

gp:AF145234

AF145234

Description

Arabidopsis thaliana NADPH:quinone oxidoreductase (NQR) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4897050_f3_44	591	2511	153	462	355	2.1e-32

Protein name

Locus Name

Acc#

acetylglutamate kinase

pir:D70477

D70477

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
50160_c1_75	592	2512	127	384	460	1.9e-42

Protein name

Locus Name

Acc#

haemoglobin-haptoglobin binding protein HhuA

gp:HIU43198

U43198

Description

Haemophilus influenzae haemoglobin-haptoglobin binding protein HhuA(hhuA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6650718_f2_40	593	2513	82	249		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6822152_c3_128	594	2514	160	483	438	3.4e-41

Protein name Locus Name Acc#

sp:RL9_ECOLI P02418

Description

50S RIBOSOMAL PROTEIN L9

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
783426_f1_15	595	2515	766	2301	2022	4.8e-209

Protein name Locus Name Acc#

sp:SYL_ECOLI

Description

P07813:P78
292:P77110

LEUCYL-TRNA SYNTHETASE, (LEUCINE--TRNA LIGASE) (LEURS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
860300_f2_29	596	2516	85	258		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9803127_c1_88	597	2517	321	966	53	0.041

Protein name Locus Name Acc#

hypothetical protein (bpi 3' region) pir:C37397 C37397

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9898513_c2_101	598	2518	527	1584	600	1.3e-88

Protein name

Locus Name

Acc#

sp:YF67_HAEIN

Description

Q57408:P96
344

PROBABLE TONB-DEPENDENT RECEPTOR HI1567 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1040887_c1_72	599	2519	301	906	601	1.8e-58

Protein name

Locus Name

Acc#

gp:AB025342

AB025342

Description

Moritella marina genes, complete cds, similar to eicosapentaenoic acid synthesis gene cluster.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10648402_f3_46	600	2520	395	1188	953	9.0e-96

Protein name

Locus Name

Acc#

sp:AROF_ECOLI

P00888

Description

SYNTHETASE) (3-DEOXY-D-ARABINO-HEPTULOSONATE 7-PHOSPHATE SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10723543_f3_48	601	2521	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10969087_f3_60	602	2522	1242	3729	2416	3.1e-286

Protein name

Locus Name

Acc#

DNA polymerase III

gp:AF062919

AF062919

Description

Pseudomonas fluorescens DNA polymerase III (dnaE) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19552252_c3_122	603	2523	111	336	238	5.3e-20

Protein name

Locus Name

Acc#

gp:D90863

Description

D90863:AB0
01340

E.coli genomic DNA, Kohara clone #407(52.4-52.8 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20180387_c2_104	604	2524	208	627	117	1.0e-05

Protein name

Locus Name

Acc#

sp:Y366_HAEIN

P43988

Description

HYPOTHETICAL PROTEIN HI0366 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20355003_f2_25	605	2525	173	522		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20486501_c3_115	606	2526	154	465	239	4.1e-20

Protein name

Locus Name

Acc#

hypothetical protein PH0336

pir:E71140

E71140

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2120263_c3_114	607	2527	200	603	217	8.9e-18

Protein name

Locus Name

Acc#

sp:YGGB_ECOLI

P11666

Description

(F286)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22131925_c3_124	608	2528	387	1164	1176	2.1e-119

Protein name

AarC

Locus Name

gp:PSU67933

Acc#

U67933

Description

Providencia stuartii AarC (aarC) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24219200_f3_59	609	2529	413	1242	872	3.5e-87

Protein name

Locus Name

sp:YCFD_HAEIN

Acc#

P44683

Description

HYPOTHETICAL PROTEIN HI0396

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24412678_f2_27	610	2530	253	762	291	1.3e-25

Protein name

Locus Name

sp:RNH2_VIBCH

Acc#

P52021

Description

RIBONUCLEASE HII, (RNASE HII) (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24423250_f3_53	611	2531	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25573802_f1_4	612	2532	446	1341	456	4.2e-43

Protein name

lipid-A-disaccharide synthase,

Locus Name

pir:E64180

Acc#

E64180

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29407800_c1_80	613	2533	403	1212	1125	5.4e-114

Protein name

Locus Name

Acc#

sp:YFGB_PSEAE

Q51385:Q51
525

Description

HYPOTHETICAL 41.7 KD PROTEIN IN PILF-NDK INTERGENIC REGION (ORF1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3145438_c1_69	614	2534	485	1458	644	1.3e-66

Protein name

Locus Name

Acc#

unknown

sp:AF003741

AF003741

Description

Escherichia coli CFT073 pathogenicity island gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33882816_c1_79	615	2535	273	822	243	1.2e-41

Protein name

Locus Name

Acc#

sp:YFCB_ECOLI

P39199:P78
252:P76939

Description

(EC 2.1.1.72)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3906293_f1_3	616	2536	110	333	146	3.0e-10

Protein name

Locus Name

Acc#

sp:YDAL_ECOLI

P76053

Description

HYPOTHETICAL 21.5 KD PROTEIN IN OGT-DBPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907568_c2_105	617	2537	395	1188	386	1.1e-35

Protein name

Locus Name

Acc#

sp:YFGL_ECOLI

P77774

Description

HYPOTHETICAL 41.9 KD PROTEIN IN XSEA-HISS INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3912818_c3_125	618	2538	425	1278	1077	6.6e-109

Protein name

Locus Name

Acc#

sp:SYH_ECOLI

P04804

Description

(HISRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3945293_c3_113	619	2539	328	987	696	1.5e-68

Protein name

Locus Name

Acc#

sp:SOHB_HAEIN

P45315

Description

POSSIBLE PROTEASE SOHB,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3946892_c3_126	620	2540	280	843	164	6.3e-12

Protein name

Locus Name

Acc#

sp:Y370_HAEIN

P43989

Description

HYPOTHETICAL PROTEIN HI0370

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3946917_f3_64	621	2541	205	618	508	1.3e-48

Protein name

Locus Name

Acc#

sp:3MGA_HAEIN

P44321

Description

GLYCOSIDASE) (TAG)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4148383_c1_83	622	2542	321	966	557	8.3e-54

Protein name

Locus Name

Acc#

hypothetical protein HP0852

pir:D64626

D64626

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4181537_c1_88	623	2543	473	1422	952	2.2e-144

Protein name

Locus Name

Acc#

sp:YFGK_ECOLI

P77254

Description

HYPOTHETICAL GTP-BINDING PROTEIN IN XSEA-HISS INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4460938_f2_37	624	2544	271	816	664	3.8e-65

Protein name

Locus Name

Acc#

O-acetylserine synthase

gp:AF010139

AF010139

Description

Azotobacter vinelandii iron-sulfur cluster assembly gene cluster, suhB, cysE2, iscS, iscU, iscA, hscB, hscA and fdx genes completecds; ndk gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5114700_c1_86	625	2545	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
52138_c1_91	626	2546	109	330	199	1.2e-15

Protein name

Locus Name

Acc#

solanesyl diphosphate synthase

gp:AB001997

AB001997

Description

Rhodobacter capsulatus DNA for solanesyl diphosphate synthase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6140680_f2_36	627	2547	300	903	187	1.9e-29

Protein name

Locus Name

Acc#

hypothetical protein b2532

pir:C65030

C65030

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
648425_c1_90	628	2548	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10378_c2_184	629	2549	85	258	251	2.2e-21

Protein name

Locus Name

Acc#

cold shock protein, CSPA

gp:VCCSPA

Y11908

Description

V.cholerae cspA gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1063510_c2_198	630	2550	175	528	208	1.5e-15

Protein name

Locus Name

Acc#

uridylyl transferase

gp:AB024601

AB024601

Description

Pseudomonas aeruginosa dapD gene for tetrahydrodipicolinateN-succinyletransferase, complete cds, strain PA01.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1175012_c1_174	631	2551	411	1236	929	3.2e-93

Protein name

Locus Name

Acc#

acetate kinase

pir:B75254

B75254

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11988812_c1_171	632	2552	161	486		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12532562_c3_232	633	2553	299	900		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12542005_f3_130	634	2554	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13001052_f1_50	635	2555	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13852337_c2_202	636	2556	351	1056	515	2.3e-49

Protein name

Locus Name

Acc#

sp:APBE_HAEIN

P44550

Description

THIAMINE BIOSYNTHESIS LIPOPROTEIN APBE PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14225300_c3_224	637	2557	123	372	440	2.1e-41

Protein name

Locus Name

Acc#

PII-protein

gp:AVU91902

U91902

Description

Azotobacter vinelandii PII-protein (glnB) and methylammoniumtransport protein (amtB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15628127_f3_98	638	2558	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15630192_c3_217	639	2559	162	489	270	2.0e-25

Protein name

Locus Name

Acc#

sp:UP04_ECOLI

Description

P39169:P76
624:P77022
:P77023

UNKNOWN PROTEIN FROM 2D-PAGE (SPOT LM6)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16597790_f3_131	640	2560	353	1062	232	2.6e-19

Protein name

Locus Name

Acc#

sp:NUC1_CUNEE

P81203

Description

NUCLEASE C1,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16603411_f2_85	641	2561	319	960	597	4.8e-58

Protein name

Locus Name

Acc#

sp:YF56_HAEIN

P45250

Description

PUTATIVE 2-HYDROXYACID DEHYDROGENASE HI1556

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
17036428_f3_138	642	2562	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23595787_c3_220	648	2568	150	453		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23718750_f2_93	649	2569	202	609	432	1.5e-40

Protein name

Locus Name

Acc#

sp:RUV_C_HAEIN

P44633

Description

JUNCTION NUCLEASE RUV_C (HOLLIDAY JUNCTION RESOLVASE RUV_C)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23727181_c2_215	650	2570	330	993		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23939008_c1_161	651	2571	123	372	141	1.0e-09

Protein name

Locus Name

Acc#

hypothetical protein

pir:T10511

T10511

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23942567_c2_212	652	2572	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23963325_f3_123	653	2573	403	1212	879	6.3e-88

Protein name

Locus Name

Acc#

sp:FADH_ECOLI

P42593

Description

A REDUCTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24353427_c2_200	654	2574	546	1641	2074	1.5e-214

Protein name

Locus Name

Acc#

sp:CH60_YEREN

P48219

Description

60) (CROSS-REACTING PROTEIN ANTIGEN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24612761_c3_246	655	2575	259	780	467	2.9e-44

Protein name

Locus Name

Acc#

sp:YMFC_HAEIN

P44827

Description

HYPOTHETICAL PROTEIN HI0694

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24648387_c1_170	656	2576	282	849	926	6.6e-93

Protein name

Locus Name

Acc#

thymidylate synthase

gp:L78665

L78665

Description

Methylobacillus flagellatum aspartate aminotransferase (aat), membrane protein (orf-1), homoserine dehydrogenase (hom), and threonine synthase (thrC) thymidylate synthase (thyA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24796885_c2_197	657	2577	268	807	801	1.2e-79

Protein name

Locus Name

Acc#

sp:AMPM_ECOLI

P07906

Description

METHIONINE AMINOPEPTIDASE, (MAP) (PEPTIDASE M)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25390711_c1_153	658	2578	414	1245	593	2.8e-60

Protein name

Locus Name

Acc#

sp:MUTY_ECOLI

P17802

Description

A/G-SPECIFIC ADENINE GLYCOSYLASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25412907_f1_37	659	2579	95	288	74	0.044

Protein name

Locus Name

Acc#

hypothetical protein

gp:AP000363

AP000363

Description

Bacteriophage VT2-Sa, complete genome sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25566577_f1_23	660	2580	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25585263_f2_64	661	2581	311	936	790	1.7e-78

Protein name

Locus Name

Acc#

diaminopimelate epimerase,

pir:S01913

B65185:S30

699:S01913

:A37841:S2

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26213386_c3_242	662	2582	404	1215	393	2.0e-36

Protein name

Locus Name

Acc#

sp:UBIH_ECOLI

P25534

Description

UBIH PROTEIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26214428_c2_201	663	2583	296	891	719	5.7e-71

Protein name

Locus Name

Acc#

sp:LGT_SALTY

Q07293

Description

PROLIPROTEIN DIACYLGLYCERYL TRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29303578_f2_74	664	2584	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29380307_c2_199	665	2585	166	501		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30268885_c3_234	666	2586	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33626535_f1_51	667	2587	141	426		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34416075_c3_231	668	2588	803	2412	1247	6.3e-127

Protein name

Locus Name

Acc#

sp:NFRX_AZOVI

P36223

Description

TRANSFERASE) (URIDYLYL REMOVING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35425918_c3_241	669	2589	176	531	302	8.7e-27

Protein name

Locus Name

Acc#

dihydrofolate reductase,

pir:S52336

S52336

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36051061_f2_78	670	2590	327	984	930	2.5e-93

Protein name

Locus Name

Acc#

probable 2

pir:G70875

G70875

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3910943_c1_146	671	2591	343	1032	1278	3.3e-130

Protein name

Locus Name

Acc#

ketol-acid reductoisomerase

gp:AF125563

AF125563

Description

Neisseria meningitidis NMB putative aconitate hydratase (acn), ornithine carbonyltransferase (argF), and ketol-acid reductoisomerase (ilvC) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3914002_f3_114	672	2592	253	762		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939063_f2_89	673	2593	469	1410	627	3.2e-61

Protein name

Locus Name

Acc#

sp:MURD_ECOLI

P14900

Description

ADDING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3947713_f1_5	674	2594	260	783	594	1.0e-57

Protein name

Locus Name

Acc#

sp:YAAA_HAEIN

P43908

Description

HYPOTHETICAL PROTEIN HI0984

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3954638_f2_63	675	2595	438	1317	1067	7.5e-108

Protein name

Locus Name

Acc#

sp:DCDA_PSEAE

P19572

Description

DIAMINOPIMELATE DECARBOXYLASE, (DAP DECARBOXYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3962885_c3_219	676	2596	181	546	486	2.8e-46

Protein name

Locus Name

Acc#

acetolactate synthase, III small
chain:acetohydroxy-acid synthase III small
chain

pir:YCEC3H

F64729:S14

386:S40591

:A01114:PS

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3992035_c1_175	677	2597	500	1503	1163	4.6e-127

Protein name

Locus Name

Acc#

sp:PTA_HAEIN

P45107

Description

PHOSPHATE ACETYLTRANSFERASE, (PHOSPHOTRANSACETYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4140881_f1_40	678	2598	467	1404	710	5.1e-70

Protein name

NorM

Locus Name

gp:AB010463

Acc#

AB010463

Description

Vibrio parahaemolyticus gene for NorM, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4147562_c1_159	679	2599	523	1572	1209	6.7e-123

Protein name

Locus Name

sp:YIFB_HAEIN

Acc#

P45049

Description

HYPOTHETICAL PROTEIN H11117

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4471887_f3_135	680	2600	415	1248	637	2.8e-62

Protein name

FtsW

Locus Name

gp:AF123260

Acc#

AF123260

Description

Coxiella burnetii FtsW (ftsW) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4720313_c1_180	681	2601	149	450	161	1.2e-10

Protein name

Locus Name

sp:METE_ECOLI

Acc#

P25665

Description

(COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4770887_f2_72	682	2602	176	531	130	2.7e-14

Protein name

hypothetical protein

Locus Name

gp:SSU18930

Acc#

Y18930

Description

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5100010_f1_7	683	2603	333	1002	581	2.4e-56

Protein name

Locus Name

Acc#

sp:XERC_HAEIN

P44818

Description

INTEGRASE/RECOMBINASE XERC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5275250_c3_235	684	2604	202	609	328	1.5e-29

Protein name

Locus Name

Acc#

Trp repressor binding protein

gp:AF067083

AF067083

Description

Vitreoscilla sp. outer membrane protein homolog gene, complete cds; Trp repressor binding protein gene, partial cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
593802_f2_71	685	2605	506	1521	433	1.1e-40

Protein name

Locus Name

Acc#

sp:RBN_HAEIN

P44608

Description

RIBONUCLEASE BN, (RNASE BN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5970933_f1_15	686	2606	105	318	249	3.6e-21

Protein name

Locus Name

Acc#

unknown protein

gp:MSGTCWPA

M15467

Description

M.tuberculosis 65 kDa antigen (cell wall protein a) gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5988327_c3_227	687	2607	927	2784	1588	4.6e-163

Protein name

Locus Name

Acc#

sp:HEPA_ECOLI

P23852:P75633

Description

RNA POLYMERASE ASSOCIATED PROTEIN (ATP-DEPENDENT HELICASE HEPA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6488910_f2_94	688	2608	66	201	85	0.0050

Protein name

Locus Name

Acc#

sp:YIHR_ECOLI

P32139

Description

HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6516885_c2_185	689	2609	213	642	140	3.5e-09

Protein name

Locus Name

Acc#

putative membrane protein.

gp:SC6D7

AL133213

Description

Streptomyces coelicolor cosmid 6D7.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
665876_c3_245	690	2610	552	1659	215	1.1e-16

Protein name

Locus Name

Acc#

sp:OMPA_BORAV

Q05146

Description

OUTER MEMBRANE PROTEIN A PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
8575_c3_236	691	2611	140	423	343	4.0e-31

Protein name

Locus Name

Acc#

sp:CH10_PSEST

O33499

Description

10)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
859388_f2_86	692	2612	342	1029	537	1.1e-51

Protein name

Locus Name

Acc#

sp:ISPA_HAEIN

P45204

Description

(FPP SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
970625_c1_145	693	2613	68	207	197	1.1e-14

Protein name

Locus Name

Acc#

sp:ILVI_ECOLI

Description

P00893:P78
045

III) (ACETOHYDROXY-ACID SYNTHASE III LARGE SUBUNIT) (ALS-III)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9957828_f2_88	694	2614	149	450	85	0.00086

Protein name

Locus Name

Acc#

transposase

gp:CETC2

Description

X59156:S88
451

Caenorhabditis elegans transposon Tc2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21736625_c2_11	695	2615	290	870	508	1.3e-48

Protein name

Locus Name

Acc#

sp:APAH_HAEIN

P44751

Description

(DIADENOSINE TETRAPHOSPHATASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26053825_f1_4	696	2616	528	1587	1002	5.8e-101

Protein name

Locus Name

Acc#

sp:DNAB_ECOLI

P03005

Description

REPLICATIVE DNA HELICASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33984677_f3_6	697	2617	382	1146	555	1.4e-53

Protein name

Locus Name

Acc#

biosynthetic alanine racemase

gp:AF165882

AF165882

Description

Pseudomonas aeruginosa biosynthetic alanine racemase (alr) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5181430_c3_14	698	2618	327	984	617	3.6e-60

Protein name

Locus Name

Acc#

sp:PDXA_ECOLI

P19624

Description

PYRIDOXAL PHOSPHATE BIOSYNTHETIC PROTEIN PDXA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7680_c3_15	699	2619	295	888	603	1.1e-58

Protein name

Locus Name

Acc#

sp:KSGA_ECOLI

P06992

Description

DIMETHYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10547156_c1_79	700	2620	1096	3291	4176	0.0

Protein name

Locus Name

Acc#

carbamoylphosphate synthetase large subunit

gp:PAU81259

U81259:L27
528

Description

Pseudomonas aeruginosa dihydrodipicolinate reductase (dapB) gene, partial cds, carbamoylphosphate synthetase small subunit (carA) and carbamoylphosphate synthetase large subunit (carB) genes, complete cds, and FtsJ homolog (ftsJ) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11915953_c1_76	701	2621	138	417	312	7.6e-28

Protein name

Locus Name

Acc#

probable oxidoreductase

pir:T35853

T35853

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13947152_f2_37	702	2622	126	381		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14094052_f1_20	703	2623	111	336	160	9.7e-12

Protein name

Locus Name

Acc#

sp:YCKK_ECOLI

Description

P45572:P75
878

HYPOTHETICAL 12.4 KD PROTEIN IN HELD-SERT INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16601077_f2_30	704	2624	93	282	103	1.1e-05

Protein name

Locus Name

Acc#

hypothetical protein

gp:SSU18930

Y18930

Description

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19562686_f3_66	705	2625	309	930	530	6.0e-51

Protein name

Locus Name

Acc#

sp:CBL_ECOLI

Description

Q47083:P76
353

TRANSCRIPTIONAL REGULATOR CBL

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19571925_c3_117	706	2626	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20313326_f2_40	707	2627	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20488827_f1_10	708	2628	558	1677	1638	2.3e-168

Protein name

sulfite reductase

Locus Name

gp:AF026066

Acc#

AF026066

Description

Pseudomonas aeruginosa sulfite reductase (cysI) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20953402_c2_103	709	2629	328	987	213	3.2e-15

Protein name

Locus Name

sp:LPPB_HAEIN

Acc#

P44833

Description

OUTER MEMBRANE ANTIGENIC LIPOPROTEIN B PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21907078_f3_55	710	2630	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22766067_f1_21	711	2631	478	1437	96	0.012

Protein name

Locus Name

sp:THDF_MYCGE

Acc#

P47254:Q49
330

Description

POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24251510_c2_88	712	2632	364	1095	746	7.8e-74

Protein name

hypothetical protein Rv3629c

Locus Name

pir:F70561

Acc#

F70561

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24259555_f2_39	713	2633	219	660	375	1.6e-34

Protein name

similar to glutathione-s-transferase

Locus Name

gp:AF036940

Acc#

AF036940:A
F081362

Description

Pseudomonas sp. U2 plasmid pWWU2, ferredoxin reductase (nagAa), salicylate-5-hydroxylase large oxygenase component (nagG), salicylate-5-hydroxylase small oxygenase component (nagH), ferredoxin (nagAb), naphthalene dioxygenase large oxygenase component (nagAc), naphthalene dioxygenase small oxygenase component (nagAd), cis-naphthalene dihydrodiol dehydrogenase (nagB), salicylaldehyde dehydrogenase

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24801562_c2_82	714	2634	554	1665	506	8.0e-73

Protein name

permease for AmpC beta-lactamase expression

Locus Name

gp:AF082985

Acc#

AF082985

Description

Pseudomonas aeruginosa permease for AmpC beta-lactamase expressionAmpG (ampG) gene, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25448412_c2_95	715	2635	98	297	186	1.7e-14

Protein name

unknown

Locus Name

gp:AF033858

Acc#

AF033858

Description

Pediococcus pentosaceus strain ATCC43200 plasmid pMD136, complete plasmid sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29429590_f2_44	716	2636	162	489	241	2.5e-20

Protein name

Locus Name

sp:VDLD_HELPY

Acc#

005729

Description

PROTEIN VDLD

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30181587_f1_9	717	2637	76	231	43	0.037

Protein name

bone morphogenetic protein 2

Locus Name

pir:A61387

Acc#

A61387

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3129637_c2_94	718	2638	323	972	577	6.3e-56

Protein name

mrr restriction system protein

Locus Name

pir:F75508

Acc#

F75508

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31375212_f3_54	719	2639	615	1848	1278	3.3e-130

Protein name

Locus Name

sp:YFBQ_ECOLI

Acc#

P77727

Description

PROBABLE AMINOTRANSFERASE YFBQ,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32878_f2_25	720	2640	349	1050	176	1.2e-10

Protein name

Locus Name

gp:ECOI10K

Acc#

D10483:J01
597:J01683
:J01706:K0

Description

E.coli K12 genome, 0-2.4min. region.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33788387_c3_108	721	2641	66	201	87	0.00053

Protein name

hypothetical protein SPCP31B10.02

Locus Name

pir:T41692

Acc#

T41692

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3915688_c1_78	722	2642	200	603	482	7.4e-46

Protein name

Locus Name

Acc#

sp:Y318_HAEIN

P43984

Description

HYPOTHETICAL PROTEIN HI0318

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
40875_f1_18	723	2643	126	381	189	8.2e-15

Protein name

Locus Name

Acc#

sp:YHEN_ECOLI

P45532

Description

HYPOTHETICAL 13.6 KD PROTEIN IN RPSL-FKPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4490902_c2_101	724	2644	166	501	522	4.3e-50

Protein name

Locus Name

Acc#

sp:GREA_ECOLI

P21346:P78
111

Description

(GREA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4536668_c3_107	725	2645	940	2823	1554	1.9e-159

Protein name

Locus Name

Acc#

sp:GLNE_ECOLI

P30870:P78
107

Description

SYNTHETASE ADENYLYLTRANSFERASE) (ATASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4572125_c1_72	726	2646	311	936	820	1.1e-81

Protein name

unknown

Locus Name

gp:PAU63816

Acc#

U63816

Description

Pseudomonas aeruginosa glnE gene, partial cds; ilvE,ADP-heptose:LPS heptosyltransferase homolog (waaF),lipopolysaccharide heptosyltransferase I homolog (waaC),glucosyltransferase I homolog (waaG), RfaP protein (waaP), and unknown protein (waaX) genes, complete cds; and inaA gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5084827_f3_48	727	2647	163	492	193	1.5e-14

Protein name

Locus Name

sp:SURA_ECOLI

Acc#

P21202:P75
630

Description

SURA), (PPIASE) (ROTAMASE C)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5287555_c2_102	728	2648	125	378	125	5.0e-08

Protein name

Locus Name

sp:YC53_HAEIN

P44139

Description

HYPOTHETICAL PROTEIN HI1253

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5322062_c1_69	729	2649	265	798	449	2.3e-42

Protein name

Locus Name

sp:MOEB_ECOLI

P12282

Description

MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6822208_c2_83	730	2650	296	891	502	5.6e-48

Protein name

Locus Name

Acc#

sp:HEMK_ECOLI

Description

P37186:Q46
754

HEMK PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6829637_f2_38	731	2651	455	1368	926	6.6e-93

Protein name

Locus Name

Acc#

sp:CYSG_ECOLI

Description

P11098:P76
685

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7117182_c3_114	732	2652	115	348	200	5.6e-16

Protein name

Locus Name

Acc#

unknown

gp:AF033858

AF033858

Description

Pediococcus pentosaceus strain ATCC43200 plasmid pMD136, complete plasmid sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7281562_c1_77	733	2653	416	1251	739	6.4e-130

Protein name

Locus Name

Acc#

sp:CARA_PSEAE

P38098

Description

PHOSPHATE SYNTHETASE GLUTAMINE CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
953181_c3_106	734	2654	450	1353	449	2.3e-42

Protein name

Locus Name

Acc#

sp:Y16S_MYCTU

P96936

Description

HYPOTHETICAL 54.8 KD PROTEIN CY20H10.28C

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
978465_f1_19	735	2655	102	309		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16985642_c2_43	736	2656	69	210	127	9.7e-08

Protein name

Locus Name

Acc#

sp:MURI_SYNY3

P73737

Description

GLUTAMATE RACEMASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
189186_c3_54	737	2657	233	702		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23628411_f1_6	738	2658	295	888	379	6.1e-35

Protein name

Locus Name

Acc#

sp:YCHB_ECOLI

P24209

Description

HYPOTHETICAL 30.9 KD PROTEIN IN HEMM-PRSA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29494003_f2_13	739	2659	672	2019	241	6.6e-17

Protein name

Locus Name

Acc#

sp:YHE3_PSEAE

P42810

Description

HYPOTHETICAL 64.8 KD PROTEIN IN HEMM-HEMA INTERGENIC REGION (ORF3)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29960761_c1_30	740	2660	468	1407	731	3.0e-72

Protein name

Locus Name

Acc#

sp:HEM1_PASMU

P95525

Description

GLUTAMYL-TRNA REDUCTASE, (GLUTR)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31291251_f2_15	741	2661	265	798	924	1.1e-92

Protein name

Locus Name

Acc#

gp:ECOPRS

M13174

Description

E.coli prs gene encoding phosphoribosylpyrophosphate synthetase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34641308_f3_23	742	2662	196	591	160	9.7e-12

Protein name

Locus Name

Acc#

sp:LOLB_PSEAE

P42812

Description

OUTER MEMBRANE LIPOPROTEIN LOLB PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4869025_f3_19	743	2663	554	1665	1876	1.4e-193

Protein name

Locus Name

Acc#

sp:ETFD_ACICA

P94132

Description

DEHYDROGENASE) (ELECTRON-TRANSFERRING-FLAVOPROTEIN DEHYDROGENASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10552153_f1_31	744	2664	74	225	168	7.1e-12

Protein name

Locus Name

Acc#

gp:AB028868

AB028868

Description

Mus musculus P4(21)n mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10722125_f2_65	745	2665	161	486	165	2.9e-12

Protein name

Locus Name

Acc#

sp:SMPA_ECOLI

P23089

Description

SMALL PROTEIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
117037_f3_138	746	2666	218	657	375	1.6e-34

Protein name

Locus Name

Acc#

sp:Y787_HAEIN

P44052

Description

HYPOTHETICAL PROTEIN HI0787

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11885927_f1_51	747	2667	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12297203_c3_236	748	2668	78	237	138	2.1e-09

Protein name

Locus Name

Acc#

hypothetical protein APE2061

pir:G72510

G72510

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12506635_f2_83	749	2669	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12697037_c2_201	750	2670	111	336	99	2.8e-05

Protein name

Locus Name

Acc#

gp:PADLDH

X70925

Description

P.acidilactici gene for d-lactate dehydrogenase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13078416_c3_233	751	2671	167	504	210	4.9e-17

Protein name

Locus Name

Acc#

ribosomal-protein-serine
N-acetyltransferase, rimL homolog ydaF

pir:F69768

F69768

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
134635_c2_226	752	2672	147	444	539	6.7e-52

Protein name

Locus Name

Acc#

ferric uptake regulator

gp:ABDNAFUR

Y14980

Description

Acinetobacter baumannii fur gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13726003_c2_196	753	2673	349	1050	736	8.9e-73

Protein name

Locus Name

Acc#

iron transport protein:protein
slr1295:protein slr1295

pir:S74691

S74691

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13870462_f3_144	754	2674	81	246	117	3.5e-07

Protein name

Locus Name

Acc#

hypothetical protein jhp1163

pir:B71840

B71840

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14553432_f2_67	755	2675	303	912	647	2.4e-63

Protein name

Locus Name

Acc#

sp:METR_SALTY

P05984

Description

TRANSCRIPTIONAL ACTIVATOR PROTEIN METR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15820312_c2_223	756	2676	867	2604	1893	2.2e-195

Protein name

Locus Name

Acc#

UspA2

sp:AF113611

AF113611

Description

Moraxella catarrhalis strain V1171 UspA2 (uspA2) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16016926_f3_137	757	2677	237	714	197	3.1e-15

Protein name

Locus Name

Acc#

growth factor-responsive protein, vascular smooth muscle:SM-20

pir:A53770

A53770

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16064061_c2_187	758	2678	397	1194	738	5.5e-73

Protein name

Locus Name

Acc#

sp:MURG_HAEIN

P45065

Description

(EC 2.4.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16171905_c2_202	759	2679	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16585933_f1_11	760	2680	765	2298	2390	4.8e-248

Protein name

Locus Name

Acc#

sp:IDH_AZOVI

P16100

Description

DECARBOXYLASE) (IDH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16678186_c3_251	761	2681	488	1467	1057	8.6e-107

Protein name

Locus Name

Acc#

hypothetical protein F32D8.4

pir:T21659

T21659

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20080051_c1_171	762	2682	299	900	330	9.4e-30

Protein name

Locus Name

Acc#

sp:YJJV_ECOLI

P39408:P78
143

Description

HYPOTHETICAL 28.9 KD PROTEIN IN OSMY-DEOC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20509628_c2_204	763	2683	378	1137	891	3.4e-89

Protein name

Locus Name

Acc#

sp:FTSZ_ECOLI

P06138:P78
047:P77857

Description

CELL DIVISION PROTEIN FTSZ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2132006_c2_218	764	2684	132	399	153	2.4e-10

Protein name

Locus Name

Acc#

hypothetical protein sll1830

pir:S75232

S75232

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22048442_f2_95	765	2685	402	1209	1010	8.2e-102

Protein name

Locus Name

Acc#

sp:DAPE_HAEIN

P44514

Description

SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE, (SDAP)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22323956_f3_130	766	2686	61	186	109	6.5e-06

Protein name

Locus Name

Acc#

hypothetical protein PH0221

pir:D71245

D71245

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22463311_f3_128	767	2687	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22734807_f1_40	768	2688	97	294		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22930306_c1_170	769	2689	354	1065	427	5.0e-40

Protein name

Locus Name

Acc#

5'-nucleotidase

gp:CL1131243

AJ131243

Description

Columba livia mRNA for 5'-nucleotidase.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23445136_f2_60	770	2690	583	1752	752	4.3e-120

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
NH(3)-dependent NAD(+) synthetase	pir:G72277	G72277

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23532300_c1_165	771	2691	78	237		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23556625_c3_245	772	2692	241	726	185	2.2e-14

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:FTSQ_ECOLI	P06136

Description

CELL DIVISION PROTEIN FTSQ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23615832_f1_16	773	2693	334	1005	125	9.1e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
lysophospholipase homolog	pir:T02661	T02661

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24111015_c3_269	774	2694	154	465	274	8.1e-24

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:RIBF_ECOLI	

Description P08391:P75621

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24219056_c1_184	775	2695	246	741	512	4.9e-49

Protein name

Locus Name

Acc#

sp:YPT5_PSEAE

P24562

Description

HYPOTHETICAL 24.5 KD PROTEIN IN PILT 5' REGION (ORF5)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24220786_f1_4	776	2696	370	1113	835	2.9e-83

Protein name

Locus Name

Acc#

sp:PILT_PSEAE

P24559

Description

TWITCHING MOBILITY PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24250928_c1_153	777	2697	78	237	207	1.0e-16

Protein name

Locus Name

Acc#

sp:YFHJ_ECOLI

P37096

Description

HYPOTHETICAL 7.7 KD PROTEIN IN PPEB-FDX INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24255260_c2_229	778	2698	115	348		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24412562_c2_189	779	2699	314	945	740	3.4e-73

Protein name

Locus Name

Acc#

sp:DDL_HAEIN

P44405

Description

D-ALANINE--D-ALANINE LIGASE, (D-ALANYLALANINE SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415875_c1_174	780	2700	322	969	832	6.0e-83

Protein name

Locus Name

Acc#

sp:HEMZ_ECOLI

Description

P23871:P78

232

SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24644577_f2_96	781	2701	535	1608	923	1.4e-92

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76051

S76051

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24813161_f3_143	732	2702	344	1035	650	1.2e-63

Protein name

Locus Name

Acc#

MsmX

gp:AB013374

AB013374

Description

Bacillus halodurans C-125 mamX, yjdA, ykoK and yvfK genes, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25579510_f3_109	783	2703	156	471	99	0.0018

Protein name

Locus Name

Acc#

myosin alpha heavy chain, masticatory muscle

pir:S33732

S33732

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26212750_c2_205	784	2704	329	990	285	7.8e-25

Protein name

Locus Name

Acc#

gp:ATAC006436

AC006436

Description

Arabidopsis thaliana chromosome II BAC F13J11 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26678567_c1_164	785	2705	63	192	88	0.00042

Protein name Locus Name Acc#
hypothetical protein 29.1 pir:S59084 S59084

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26813135_c2_192	786	2706	524	1575	1287	3.7e-131

Protein name Locus Name Acc#
alkyl hydroperoxide reductase, F52A protein pir:D64794 D64794

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
273427_c3_263	787	2707	224	675	583	1.5e-56

Protein name Locus Name Acc#
sp:DEDA_ECOLI P09548

Description

DEDA PROTEIN (DSG-1 PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29337825_f2_62	788	2708	67	204	131	1.2e-08

Protein name Locus Name Acc#
sp:YPT1_PSEAE P24560

Description

HYPOTHETICAL 17.0 KD PROTEIN IN PILT 5' REGION (ORF1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31252614_c3_231	789	2709	68	207	85	0.0054

Protein name Locus Name Acc#
glutathione synthetase gp:D88540 D88540

Description

Synechococcus sp. DNA for glutathione synthetase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3236505_c2_217	790	2710	119	360	127	1.7e-07

Protein name

hypothetical protein sll1830

Locus Name

pir:S75232

Acc#

S75232

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32593750_f1_27	791	2711	366	1101	1382	3.1e-141

Protein name

Locus Name

sp:RECA_ACICA

Acc#

P42438

Description

RECA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33788286_c2_188	792	2712	493	1482	1448	3.2e-148

Protein name

UDP-N-acetylmuramate:L-alanine ligase MurC

Locus Name

gp:AF110740

Acc#

AF110740

Description

Pseudomonas aeruginosa UDP-N-acetylmuramate:L-alanine ligase MurC(murC) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34040777_c1_169	793	2713	196	591	93	0.00011

Protein name

Locus Name

sp:PPDD_ECOLI

Acc#

P36647

Description

PREPILIN PEPTIDASE DEPENDENT PROTEIN D PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34159412_f1_53	794	2714	330	993	497	1.9e-47

Protein name

oxidative stress transcriptional regulator

Locus Name

gp:XCU94336

Acc#

U94336

Description

Xanthomonas campestris alkyl hydroperoxide reductase subunits C(ahpC) and F(ahpF) and oxidative stress transcriptional regulator(oxyR) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35276891_f3_132	795	2715	80	243	88	0.00042

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein	pir:D75542	D75542

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907311_f3_110	796	2716	74	225		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3928750_c3_242	797	2717	298	897	412	1.9e-38

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YHIR_HAEIN	P31777

Description

HYPOTHETICAL PROTEIN HI0441 (ORFJ)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3940943_f2_59	798	2718	118	357	93	0.00012

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YGFE_ECOLI	P45580

Description

HYPOTHETICAL 12.6 KD PROTEIN IN PEPP-SSR INTERGENIC REGION (O109)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3947318_f3_116	799	2719	276	831	1038	8.9e-105

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:DAPD_MYCBO	P56220

Description

(THP SUCCINYLTRANSFERASE) (TETRAHYDROPICOLINATE SUCCINYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4017832_f2_85	800	2720	211	636	525	2.0e-50

Protein name

DedA family protein

Locus Name

pir:B75253

Acc#

B75253

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4023342_c1_186	801	2721	215	648	145	3.8e-10

Protein name

Locus Name

sp:YGFB_ECOLI

Acc#

P25533

Description

(F194)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
402336_f2_89	802	2722	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4140943_f2_73	803	2723	157	474		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4331430_f1_28	804	2724	313	942	124	2.4e-16

Protein name

Locus Name

sp:RECX_VIBCH

Acc#

Q56647

Description

REGULATORY PROTEIN RECX

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4332837_c3_256	805	2725	105	318	149	6.7e-10

Protein name Locus Name Acc#
hypothetical protein sll1830 pir:S75232 S75232

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4348813_c3_259	806	2726	350	1053	1035	1.8e-104

Protein name Locus Name Acc#
sp:GCP_HAEIN P43764

Description

(GLYCOPROTEASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4694427_f3_114	807	2727	362	1089	884	1.9e-88

Protein name Locus Name Acc#
sp:LIPA_HAEIN P44463

Description

LIPOLIC ACID SYNTHETASE (LIP-SYN) (LIPOATE SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4773260_f2_79	808	2728	79	240		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4798536_c2_191	809	2729	212	639	685	2.3e-67

Protein name Locus Name Acc#
alkyl hydroperoxide reductase subunit C gp:AF129406 AF129406

Description

Bacteroides fragilis alkyl hydroperoxide reductase subunit C (ahpC) and alkyl hydroperoxide reductase subunit F (ahpF) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
4824062_c2_200	810	2730	273	822	353	3.4e-32

Protein name

Locus Name

Acc#

sp:PSS_HELPY

Description

Q48269:007
681

(PHOSPHATIDYLSELINE SYNTHASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6110943_c2_203	811	2731	435	1308	303	3.5e-26

Protein name

Locus Name

Acc#

sp:FTSA_BUCAP

051928

Description

CELL DIVISION PROTEIN FTSA

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
659686_c2_210	812	2732	278	837	485	3.5e-46

Protein name

Locus Name

Acc#

sp:YGDL_HAEIN

Description

Q57097:005
009

HYPOTHETICAL PROTEIN HI0118

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
6754081_c3_235	813	2733	254	765	169	1.1e-12

Protein name

Locus Name

Acc#

hypothetical protein MTH939

pir:G69225

G69225

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
681453_f3_127	814	2734	84	255	76	0.038

Protein name

Locus Name

Acc#

sp:YXEH_BACSU

P54947

Description

HYPOTHETICAL 30.2 KD PROTEIN IN IDH-DEOR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
682641_f1_42	815	2735	86	261	100	2.2e-05

Protein name

hypothetical protein PH0217

Locus Name

pir:G71244

Acc#

G71244

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7222187_f1_35	816	2736	245	738	287	3.4e-25

Protein name

conserved hypothetical protein ykrA

Locus Name

pir:C69862

Acc#

C69862

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781563_c2_227	817	2737	113	342	265	7.3e-23

Protein name

Locus Name

sp:YPT6 PSEAE

Acc#

P24564

Description

HYPOTHETICAL 19.5 KD PROTEIN IN PILT REGION (ORF6)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
812535_f1_43	818	2738	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10625252_f1_3	819	2739	581	1746	1790	1.8e-184

Protein name

Locus Name

sp:SYP_HAEIN

Acc#

P43830

Description

PROLYL-TRNA SYNTHETASE, (PROLINE--TRNA LIGASE) (PRORS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20496062_c2_30	820	2740	408	1227	1522	4.6e-156

Protein name

Locus Name

Acc#

sp:TRPB_ACICA

P16706

Description

TRYPTOPHAN SYNTHASE BETA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22847180_c1_17	821	2741	213	642	568	5.7e-55

Protein name

Locus Name

Acc#

sp:YADG_ECOLI

P36879

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YADG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642268_c3_37	822	2742	213	642	510	7.9e-49

Protein name

Locus Name

Acc#

sp:TRPF_ACICA

P16923

Description

N-(5'-PHOSPHORIBOSYL)ANTHRANILATE ISOMERASE, (PRAI)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24814125_c2_31	823	2743	285	858	541	4.1e-52

Protein name

Locus Name

Acc#

tryptophan synthase alpha chain

gp:AF107094

AF107094

Description

Rhodobacter sphaeroides thiamine biosynthetic protein (thi) gene,partial cds; and tryptophan synthase alpha chain (trpA) gene,complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30727194_c2_24	824	2744	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3941642_c2_25	825	2745	100	303	224	1.6e-18

Protein name

Locus Name

Acc#

sp:YADG_ECOLI

P36879

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YADG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4181557_c1_19	826	2746	281	846	553	2.2e-53

Protein name

Locus Name

Acc#

sp:YQCD_ECOLI

Q46920

Description

HYPOTHETICAL 32.6 KD PROTEIN IN SYD-SDAC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4426338_c2_26	827	2747	260	783	744	1.3e-73

Protein name

Locus Name

Acc#

sp:YADH_ECOLI

P36880:P75
657

Description

HYPOTHETICAL 28.5 KD PROTEIN IN HPT-PAND INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5120412_c3_32	828	2748	186	561	196	1.5e-15

Protein name

Locus Name

Acc#

cytochrome c5

gp:AVU94420

U94420

Description

Azotobacter vinelandii aldehyde dehydrogenase (aldh) gene, partial cds, cytochrome c5 (cycB) gene, complete cds, and xanthinephosphoribosyltransferase-like protein (xrpt) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7031312_c3_33	829	2749	66	201	129	7.5e-08

Protein name

Locus Name

Acc#

sp:YADG_ECOLI

P36879

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YADG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11198430_c3_60	830	2750	692	2079	3292	0.0

Protein name

lactoferrin binding protein B

Locus Name

gp:AF043131

Acc#

AF043131

Description

Moraxella catarrhalis strain 4223 lactoferrin binding protein B(lbpB) and lactoferrin binding protein A (lbpA) genes, completecds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16128933_c2_53	831	2751	159	480	377	9.9e-35

Protein name

apolipoprotein N-acyltransferase

Locus Name

gp:AF038595

Acc#

AF038595

Description

Pseudomonas aeruginosa apolipoprotein N-acyltransferase (cute)gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19704378_c3_64	832	2752	606	1821	1227	8.3e-125

Protein name

unknown

Locus Name

gp:AF043132

Acc#

AF043132

Description

Moraxella catarrhalis strain Q8 lactoferrin binding protein B(lbpB) and lactoferrin binding protein A (lbpA) genes, completecds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24337826_c3_67	833	2753	718	2157	278	2.9e-21

Protein name

hypothetical protein K08H10.2a

Locus Name

pir:T23512

Acc#

T23512:T24
613

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34164812_c2_54	834	2754	198	597	712	1.6e-80

Protein name

lactoferrin binding protein B

Locus Name

gp:AF043133

Acc#

AF043133

Description

Moraxella catarrhalis strain VH19 lactoferrin binding protein B(lbpB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35837503_f2_26	835	2755	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35945257_c1_46	836	2756	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3906263_c2_55	837	2757	1003	3012	5252	0.0

Protein name

Locus Name

Acc#

lactoferrin binding protein A

gp:AF043131

AF043131

Description

Moraxella catarrhalis strain 4223 lactoferrin binding protein B(lbpB) and lactoferrin binding protein A (lbpA) genes, completecds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3945388_f3_30	838	2758	413	1242	1219	5.9e-124

Protein name

Locus Name

Acc#

beta-ketoacyl-ACP synthase I

gp:PAU70470

U70470

Description

Pseudomonas aeruginosa lemA-type sensor kinase/response regulatorhomolog gene, partial cds, beta-hydroxy-ACP dehydrase (fabA) andbeta-ketoacyl-ACP synthase I (fabB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4005250_c3_68	839	2759	163	492	572	2.1e-55

Protein name

ribosomal protein S12:streptomycin
resistance protein

Locus Name

pir:A42939

Acc#

B42939:A42

939:H64078

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4093767_c3_63	840	2760	544	1635	2854	3.2e-297

Protein name

unknown

Locus Name

gp:AF043131

Acc#

AF043131

Description

Moraxella catarrhalis strain 4223 lactoferrin binding protein B (lbpB) and
lactoferrin binding protein A (lbpA) genes, completedcds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4804632_f2_17	841	2761	485	1458	572	2.1e-55

Protein name

Locus Name

sp:PABB_SALTY

Acc#

P12680

Description

PARA-AMINO BENZOATE SYNTHASE COMPONENT I, (ADC SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1018_c1_12	842	2762	229	690	163	4.7e-12

Protein name

Locus Name

gp:BPMB78P21

Acc#

X87092

Description

Bacteriophage MB78 ORFs p21, p11.5, p26 & p28.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12303577_c1_11	843	2763	105	318		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19557893_c2_17	844	2764	126	381		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20038305_c2_15	845	2765	75	228		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2134555_c1_13	846	2766	169	510		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23470625_c3_19	847	2767	189	570	287	5.9e-25

Protein name

Locus Name

Acc#

gp:RP4TRANOKF

L10330

Description

Plasmid RP4 traN gene, complete cds; traO gene, complete cds; kfrAgene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23632818_c3_25	848	2768	97	291		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31555_c3_20	849	2769	333	1002	225	2.0e-17
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
coat protein			pir:S58142			S58142:T42 283
<u>Description</u>						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34381286_c3_21	850	2770	140	423		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
34485637_c3_22	851	2771	137	414		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3907963_c3_23	852	2772	81	246		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4804763_c2_16	853	2773	122	369		
<u>Protein name</u>			<u>Locus Name</u>			<u>Acc#</u>
<u>Description</u>						
NO-HIT						

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6928168_c2_18	854	2774	308	927		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12625177_f1_2	855	2775	148	447	435	7.0e-41

Protein name Locus Name Acc#

sp:DKSA_ECOLI P18274

Description

DNAK SUPPRESSOR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14241635_c2_80	856	2776	130	393		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14876881_c2_82	857	2777	256	771	350	7.2e-32

Protein name Locus Name Acc#

sp:FMCH_BACNO P17419

Description

POSSIBLE FIMBRIAL ASSEMBLY PROTEIN FIMC (SEROGROUP H1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16181301_f3_63	858	2778	203	612	126	2.6e-06

Protein name Locus Name Acc#

sp:YGGH_ECOLI P32049

Description

HYPOTHETICAL 27.3 KD PROTEIN IN ANSB-MUTY INTERGENIC REGION (F239)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16898413_c1_77	859	2779	100	303	286	9.1e-24

Protein name

Locus Name

Acc#

sp:Y712_HAEIN

P44836

Description

PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21517252_f1_3	860	2780	621	1866	1417	6.1e-145

Protein name

Locus Name

Acc#

sp:UVRC_PSEFL

P32966

Description

EXCINUCLEASE ABC SUBUNIT C

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22004587_f2_24	861	2781	333	1002	436	5.5e-41

Protein name

Locus Name

Acc#

sp:YADB_ECOLI

P27305:P75
662

Description

HYPOTHETICAL 34.9 KD PROTEIN IN PCNB-DKSA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23597187_f3_61	862	2782	769	2310	539	3.0e-100

Protein name

Locus Name

Acc#

sp:PRIA_RHORU

P05445

Description

PRIMOSOMAL PROTEIN N' (REPLICATION FACTOR Y)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23865681_f3_58	863	2783	739	2220	789	2.2e-78

Protein name

Locus Name

Acc#

sp:SPOT_HAEIN

P43811

Description

((PPGPP)ASE) (PENTA-PHOSPHATE GUANOSINE-3'-PYROPHOSPHOHYDROLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24412817_c2_92	864	2784	84	255		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2510887_c1_76	865	2785	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26594686_f1_14	866	2786	215	648	355	2.1e-32

Protein name

Locus Name

Acc#

sp:YICG_ECOLI

P31432:P76
720

Description

HYPOTHETICAL 22.0 KD PROTEIN IN RPH-GMK INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29304827_c2_94	867	2787	63	192	286	9.1e-24

Protein name

Locus Name

Acc#

sp:Y712_HAEIN

P44836

Description

PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29484418_c2_95	868	2788	566	1701	710	1.6e-118

Protein name

Locus Name

Acc#

methyltransferase

gp:AF060119

AF060119

Description

Pasteurella haemolytica methyltransferase (mod) and restrictionendonuclease (res) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30281911_c3_114	869	2789	79	240	286	9.1e-24

Protein name

Locus Name

Acc#

sp:Y712_HAEIN

P44836

Description

PROBABLE TONB-DEPENDENT RECEPTOR HI0712 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34017010_f2_35	870	2790	307	924	708	8.3e-70

Protein name

Locus Name

Acc#

hypothetical protein b2431

pir:F65017

F65017

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34407905_c2_93	871	2791	460	1383	1801	1.2e-185

Protein name

Locus Name

Acc#

L-2,4-diaminobutyrate:2-ketoglutarate

gp:AB001599

AB001599

Description

Acinetobacter baumannii DNA for L-2,4-diaminobutyrate:2-ketoglutarate 4-aminotransferase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34641550_c3_119	872	2792	186	561	126	1.2e-07

Protein name

Locus Name

Acc#

sp:AIL_YEREN

P16454

Description

ATTACHMENT INVASION LOCUS PROTEIN PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3923818_f2_34	873	2793	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4306455_c1_65	874	2794	323	972	122	4.9e-07

Protein name

Locus Name

Acc#

sp:FMP1_PSEAE

P17838

Description

FIMBRIAL PROTEIN PRECURSOR (PILIN) (STRAIN P1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4329518_f3_56	875	2795	212	639	541	4.1e-52

Protein name

Locus Name

Acc#

sp:KGUA_ECOLI

P24234

Description

GUANYLATE KINASE, (GMP KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4428413_c1_78	876	2796	517	1554	2128	2.8e-220

Protein name

Locus Name

Acc#

L-2,4-diaminobutyrate decarboxylase

gp:ACCL24DD

D55724

Description

Acinetobacter baumannii gene for L-2,4-diaminobutyrate decarboxylase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4538558_f3_51	877	2797	270	813	611	1.6e-59

Protein name

Locus Name

Acc#

hypothetical protein

gp:PPPAL1

X74218

Description

Pseudomonas putida ruvB, tolQ, tolR, tolA, tolB and oprL genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4570318_f3_44	878	2798	228	687	448	3.0e-42

Protein name

Locus Name

Acc#

sp:GPH_HAEIN

P44755

Description

PHOSPHOGLYCOLATE PHOSPHATASE, (PGP)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4902305_c2_96	879	2799	869	2610	2182	5.3e-226

Protein name

restriction endonuclease

Locus Name

gp:AF060119

Acc#

AF060119

Description

Pasteurella haemolytica methyltransferase (mod) and restrictionendonuclease (res) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4964000_f3_57	880	2800	95	288	187	1.3e-14

Protein name

Locus Name

sp:RPOZ_HAEIN

Acc#

P43740

Description

OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5079408_f3_60	881	2801	151	456	367	1.1e-33

Protein name

hypothetical protein 1 (vnfA 5' region)

Locus Name

pir:B44514

Acc#

B44514

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5080293_c2_89	882	2802	592	1779	1142	8.5e-116

Protein name

Locus Name

sp:RECJ_HAEIN

Acc#

P45112

Description

SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5339762_c3_109	883	2803	325	978	1184	3.0e-120

Protein name

LytB

Locus Name

gp:AF027189

Acc#

AF027189

Description

Acinetobacter sp. BD413 lytB, comB, comC, comE, and comF genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
97582_f3_42	884	2804	289	870	291	1.3e-25

Protein name

Locus Name

Acc#

sp:ICC_ECOLI

P36650

Description

ICC PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13673437_c2_39	885	2805	597	1791	150	3.5e-13

Protein name

Locus Name

Acc#

putative terminase

gp:AF147978

AF147978

Description

Bacteriophage D3 putative terminase, putative portal protein, putative ClpP protease, and major head protein genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14181292_c3_43	886	2806	101	306		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19953125_c2_36	887	2807	215	648		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25665952_c1_33	888	2808	128	387	88	0.0036

Protein name

Locus Name

Acc#

1.7 protein

gp:BPH251805

AJ251805

Description

Bacteriophage phi-Ye03-12 complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26675311_c2_37	889	2809	107	324	145	3.8e-10

Protein name

hypothetical protein

Locus Name

gp:XNEI33022

Acc#

AJ133022

Description

Xenorhabdus nematophilus proviral ORF1 to ORF8.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32657262_c2_35	890	2810	150	453	209	6.7e-18

Protein name

DNA primase

Locus Name

pir:C41830

Acc#

C41830

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3941887_c1_32	891	2811	185	558	88	0.019

Protein name

Locus Name

gp:PFA53C6

Acc#

X17490

Description

Plasmodium falciparum mRNA for asparagine-rich antigen (clone53C6).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5916253_c1_28	892	2812	257	774	259	3.1e-22

Protein name

Locus Name

sp:YE22_HAEIN

Acc#

P44193

Description

HYPOTHETICAL PROTEIN HI1422

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
900215_c3_41	893	2813	797	2394	330	4.7e-27

Protein name

putative DNA primase

Locus Name

gp:AF139719

Acc#

AF139719

Description

Klebsiella oxytoca plasmid pACM1 putative DNA primase (pri) gene, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10959627_f2_14	894	2814	294	885	513	3.8e-49

Protein name

Locus Name

Acc#

sp:YBEX_ECOLI

P77392

Description

HYPOTHETICAL 33.3 KD PROTEIN IN CUTE-ASNB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1178127_f3_20	895	2815	963	2892	2605	1.9e-281

Protein name

Locus Name

Acc#

SecA

gp:AB012226

AB012226

Description

Vibrio alginolyticus gene for SecA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12298468_f1_13	896	2816	102	309	82	0.017

Protein name

Locus Name

Acc#

probable membrane protein L549.12

pir:T02800

T02800

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12985393_f3_16	897	2817	270	813	537	1.1e-51

Protein name

Locus Name

Acc#

sp:PEPD_HAEIN

P44817

Description

(PEPTIDASE D)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14538262_c2_40	898	2818	69	210	109	2.5e-06

Protein name

Locus Name

Acc#

hypothetical protein APE0458

pir:A72741

A72741

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14548260_c1_34	899	2819	244	735	265	7.3e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein D1022.4	pir:T34190	T34190

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21640900_f1_8	900	2820	442	1329	1361	5.3e-139

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:GSA_PSEAE	P48247

Description

(GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24609561_c3_56	901	2821	241	726	147	2.4e-19

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:UP14_ECOLI	

Description P39179:Q46826

UNKNOWN PROTEIN FROM 2D-PAGE (SPOT PR51)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36329806_f1_2	902	2822	80	243	60	0.019

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
thyroid hormone sulfotransferase, B2	pir:JC5885	JC5885

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4188811_f1_6	903	2823	159	480	310	1.2e-27

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
conserved hypothetical protein	pir:T03501	T03501

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4336018_f1_7	904	2824	115	348	349	9.1e-32

Protein name

Locus Name

Acc#

sp:PHNA_ECOLI

P16680

Description

PHNA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4689143_f2_15	905	2825	175	528	132	9.0e-08

Protein name

Locus Name

Acc#

apolipoprotein N-acyltransferase

gp:AF038595

AF038595

Description

Pseudomonas aeruginosa apolipoprotein N-acyltransferase (cutE)gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5205312_f3_21	906	2826	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22382752_c1_11	907	2827	117	354	100	2.2e-05

Protein name

Locus Name

Acc#

hypothetical protein

pir:T10511

T10511

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26251376_c1_8	908	2828	82	249		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35188942_c3_14	909	2829	255	768	248	4.6e-21

Protein name

hypothetical protein slr1971

Locus Name

pir:S75639

Acc#

S75639

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35337805_c1_10	910	2830	185	558	152	5.9e-12

Protein name

sulfate transporter

Locus Name

gp:D89631

Acc#

D89631

Description

Arabidopsis thaliana mRNA for sulfate transporter, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35801416_f1_1	911	2831	255	768	379	6.1e-35

Protein name

Locus Name

sp:RLUA_ECOLI

Acc#

P39219

Description

(PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4328403_c2_13	912	2832	109	330	191	5.1e-15

Protein name

BolA protein

Locus Name

gp:PFL243174

Acc#

AJ243174

Description

Pseudomonas fluorescens partial Fumarase C gene, bolA gene andORF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4572206_c1_9	913	2833	380	1143	391	1.5e-35

Protein name

sulfate transporter

Locus Name

gp:AB008782

Acc#

AB008782

Description

Arabidopsis thaliana mRNA for sulfate transporter, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16990667_f1_7	914	2834	61	186	109	8.8e-06

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hemV protein	pir:S54440	S54440

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19534511_c3_45	915	2835	70	213		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19573425_c1_31	916	2836	150	453		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20408375_c2_34	917	2837	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20930_c3_42	918	2838	144	435	87	0.0070

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ATPZ_PSEPU	P25760

Description

ATP SYNTHASE PROTEIN I

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35159406_c3_39	924	2844	65	198	65	0.0045

Protein name

extensin homolog F2401.18

Locus Name

pir:T01456

Acc#

T01456

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3953587_f3_23	925	2845	174	525	236	8.6e-20

Protein name

Locus Name

sp:ZUR_ECOLI

Acc#

P32692:P76
784

Description

ZINC UPTAKE REGULATION PROTEIN (ZINC UPTAKE REGULATOR)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4120425_c1_29	926	2846	202	609	268	3.5e-23

Protein name

Locus Name

sp:ATPD_VIBAL

P12987

Description

ATP SYNTHASE DELTA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4332943_c1_27	927	2847	84	255	261	1.9e-22

Protein name

Locus Name

sp:ATPL_HAEIN

P43721

Description

(DICYCLOHEXYLCARBODIIMIDE-BINDING PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
56333_c3_44	928	2848	309	930	894	1.6e-89

Protein name

Locus Name

sp:ATPG_ECOLI

P00837:P00
838

Description

ATP SYNTHASE GAMMA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7056441_c2_38	929	2849	139	417	300	1.4e-26

Protein name

Locus Name

Acc#

sp:ATPE_HAEIN

P43718

Description

ATP SYNTHASE EPSILON CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9928433_f2_17	930	2850	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3235950_c2_28	931	2851	561	1686	2096	6.8e-217

Protein name

Locus Name

Acc#

urocanase

gp:PSEHUTUU

M33923:M28
362

Description

Pseudomonas putida urocanase (hutU) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3940938_c2_30	932	2852	357	1074	366	1.4e-33

Protein name

Locus Name

Acc#

sp:HUTG_KLEAE

P19452

Description

(HISTIDINE UTILIZATION PROTEIN G) (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3953181_c3_34	933	2853	434	1305	1007	1.7e-101

Protein name

Locus Name

Acc#

gp:YP102KB

AL031866

Description

Yersinia pestis 102 kbases unstable region: from 1 to 119443.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4822181_f3_14	934	2854	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
789037_c3_33	935	2855	525	1578	1486	3.0e-152

Protein name

Locus Name

Acc#

histidine ammonia-lyase, :histidase

pir:A35251

A35251:S39
381

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
828942_f1_1	936	2856	296	891	180	7.0e-12

Protein name

Locus Name

Acc#

sp:YYAM_BACSU

P37511

Description

HYPOTHETICAL 32.9 KD PROTEIN IN TETB-EXOA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10978400_c3_163	937	2857	253	762	186	1.7e-14

Protein name

Locus Name

Acc#

sp:HEM4_PSEAE

P48246

Description

)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1259626_c2_127	938	2858	614	1845	1756	7.3e-181

Protein name

Locus Name

Acc#

sp:YA51_HAEIN

Q57180:O05
043

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN HI1051

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12672305_c2_140	939	2859	110	333	144	4.8e-10

Protein name

Locus Name

Acc#

sp:YGGX_HAEIN

P44048

Description

HYPOTHETICAL PROTEIN HI0760

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13131890_f3_71	940	2860	169	510	147	2.7e-10

Protein name

Locus Name

Acc#

sp:DSBC_ERWCH

P39691

Description

THIOL:DISULFIDE INTERCHANGE PROTEIN DSBC PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14847290_f3_89	941	2861	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15875832_f3_92	942	2862	75	228		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16493891_c3_165	943	2863	118	357		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16610052_c3_183	944	2864	93	282		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1957701_f1_30	945	2865	277	834	329	1.2e-29

Protein name

Locus Name

Acc#

sp:GRPE_HAEIN

P43732

Description

GRPE PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19720930_f3_74	946	2866	276	831	597	4.8e-58

Protein name

Locus Name

Acc#

sp:DAPB_ECOLI

P04036

Description

DIHYDRODIPICOLINATE REDUCTASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21489390_f2_59	947	2867	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21689063_f1_10	948	2868	414	1245	328	1.5e-29

Protein name

Locus Name

Acc#

SrpJ

sp:AF176824

AF176824

Description

Synechococcus PCC7942 plasmid pANL O-acetylserine(Thiol)-lyase SrpD (srpD), gamma-glutamyltranspeptidase SrpE (srpE), alpha-helicalcoiled-coil protein SrpF (srpF), SrpJ (srpJ), ATP-binding protein of ABC transporter SrpK (srpK), membrane lipoprotein SrpL (srpL), and cytoplasmic membrane protein SrpM (srpM) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22042177_f2_65	949	2869	493	1482	1203	2.9e-122

Protein name

argininosuccinate lyase argH

Locus Name

pir:C69589

Acc#

C69589

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22070191_f1_5	950	2870	409	1230	486	2.8e-46

Protein name

cystathionine-gamma-lyase

Locus Name

gp:AF180145

Acc#

AF180145

Description

Zymomonas mobilis GTP-binding protein CgpA (cgpA), 60KDinner-membrane protein yidC (yidC), hypothetical protein, glutamine-pyruvate aminotransferase gltB (gltB), glutamate synthasesmall subunit gltS (gltS), undecaprenol kinase udk (udk), hypothetical protein, NADH dehydrogenase, hypothetical protein; zml2orf5, hypothetical protein, aspartate aminotransferase A, beta-hydroxysteroid dehydrogenase, phosphomannomutase pmm

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22922082_c2_138	951	2871	319	960		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
234701_c3_187	952	2872	73	222	115	5.1e-07

Protein name

extensin

Locus Name

pir:S22697

Acc#

S22697:S21
006

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23572127_f1_31	953	2873	636	1911	2307	3.0e-239

Protein name

Locus Name

Acc#

sp:DNAK_FRATU

P48205

Description

DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23909688_f3_77	954	2874	466	1401	456	4.2e-43

Protein name

rubredoxin--NAD+ reductase, :hypothetical protein hydA 3'-region

Locus Name

pir:C65051

Acc#

C65051

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24073762_c3_158	955	2875	220	663	681	6.0e-67

Protein name

AvtA

Locus Name

gp:AF014804

Acc#

AF014804

Description

Neisseria meningitidis PglB (pglB), PglC (pglC), PglD (pglD), andAvtA (avtA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24100465_f2_46	956	2876	321	966	639	1.3e-64

Protein name

intrinsic membrane protein

Locus Name

gp:AB000100

Acc#

AB000100

Description

Synechococcus sp. DNA for intrinsic membrane protein, malK-likeprotein, cyanase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24391877_c1_109	957	2877	329	990	927	5.1e-93

Protein name

Locus Name

sp:HEM3_ECOLI

Acc#

P06983:P78125

Description

SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24417807_f3_76	958	2878	185	558	263	1.2e-22

Protein name

Mip

Locus Name

gp:S71704

Acc#

S71704

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24619003_f3_79	959	2879	287	864	625	5.2e-61

Protein name

Locus Name

Acc#

sp:NRTC_SYNY3

P73450

Description

NITRATE TRANSPORT ATP-BINDING PROTEIN NRTC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26053250_c1_112	960	2880	268	807		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26053250_c2_134	961	2881	116	351		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26362680_c2_129	962	2882	296	891	480	1.2e-45

Protein name

Locus Name

Acc#

sp:YJFH_HAEIN

P44906

Description

HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE HI0860,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2928382_f2_40	963	2883	323	972	895	1.3e-89

Protein name

Locus Name

Acc#

sodium-dependent transporter homolog yocS

pir:E69902

E69902

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29339432_c3_166	964	2884	322	969	92	4.2e-06

Protein name

hypothetical protein b2755

Locus Name

pir:G65056

Acc#

G65056

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29962837_c3_181	965	2885	288	867	117	9.9e-13

Protein name

Locus Name

sp:DNAJ_SYNP7

Acc#

P50026

Description

DNAJ PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32629186_c2_139	966	2886	223	672		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3307_f2_47	967	2887	119	360	349	9.1e-32

Protein name

Locus Name

sp:YADR_HAEIN

Acc#

P45344

Description

HYPOTHETICAL PROTEIN HI1723

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34492161_c3_168	968	2888	353	1062		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3940925_c3_182	969	2889	341	1026	466	3.7e-44

Protein name

Locus Name

Acc#

sp:YHET_ECOLI

P45524

Description

HYPOTHETICAL 38.5 KD PROTEIN IN KIFB-PRKB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4095443_c3_170	970	2890	161	486	147	2.3e-10

Protein name

Locus Name

Acc#

hypothetical protein Rv0163

pir:G70903

G70903

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4187538_f2_50	971	2891	473	1422	1141	1.1e-115

Protein name

Locus Name

Acc#

sp:MPL_HAEIN

P43948

Description

LIGASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4328135_f1_13	972	2892	474	1425	812	7.9e-81

Protein name

Locus Name

Acc#

periplasmic substrate binding protein

gp:AF001333

AF001333

Description

Synechococcus PCC7942 periplasmic substrate binding protein (cynA), integral membrane protein (cynB) and ATP-binding protein (cynD) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4328965_f3_99	973	2893	132	399	282	1.2e-24

Protein name

Locus Name

Acc#

sp:Y117_HAEDU

O30825

Description

HYPOTHETICAL PROTEIN HYPO117

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4423318_c3_160	974	2894	626	1881	2307	3.0e-239

Protein name

93% identity over 631 amino acids with E. coli

Locus Name

gp:STYSTMF1

Acc#

AF170176

Description

Salmonella typhimurium fragment STMF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4454512_f1_32	975	2895	111	336	113	9.3e-07

Protein name

Locus Name

sp:Y173_HAEIN

Acc#

P43960

Description

HYPOTHETICAL PROTEIN HI0173

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4548188_f1_38	976	2896	421	1266	1342	5.4e-137

Protein name

Locus Name

sp:DADA_ECOLI

Acc#

P29011

Description

D-AMINO ACID DEHYDROGENASE SMALL SUBUNIT,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5119127_c2_153	977	2897	651	1956	1464	6.4e-150

Protein name

Locus Name

sp:YHES_ECOLI

Acc#

P45535

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YHES

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6727086_f1_17	978	2898	563	1692	879	6.3e-88

Protein name

putative gamma-glutamylcysteine synthetase

Locus Name

gp:PSP243941

Acc#

AJ243941

Description

Pseudomonas sp. strain HR199 partial vanB, fdh, gcs, ehyA and ehyBgenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
673253_f3_72	979	2899	407	1224	1146	3.2e-116

Protein name

Locus Name

Acc#

sp:DNAJ_SALTY

Q60004

Description

DNAJ PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6854677_c3_167	980	2900	462	1389		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
801452_f2_60	981	2901	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
884712_c1_113	982	2902	1191	3576	79	0.0031

Protein name

Locus Name

Acc#

hypothetical protein PH1246

pir:A71069

A71069

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
915633_c1_115	983	2903	74	225		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9766888_f1_18	984	2904	182	549	229	4.8e-19

Protein name

Locus Name

Acc#

sp:YA21_PSEAE

P21482

Description

HYPOTHETICAL 17.8 KD PROTEIN IN ALGR2 5'REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10329680_f1_3	985	2905	544	1635	587	5.5e-57

Protein name

Locus Name

Acc#

gp:PSEOPRC

D28119

Description

Pseudomonas aeruginosa oprC gene for outer membrane protein C,complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10626550_c3_128	986	2906	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11017010_c3_139	987	2907	247	744		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12894752_f1_13	988	2908	69	210	84	0.016

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:A72221

A72221

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
13759627_c3_138	989	2909	88	267		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14633433_f3_55	990	2910	122	369		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
16023402_c3_125	991	2911	887	2664	1410	6.3e-160

Protein name Locus Name Acc#

sp:FTSK_COXBU P39920

Description

CELL DIVISION PROTEIN FTSK HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19537930_f1_1	992	2912	97	294	116	4.5e-07

Protein name Locus Name Acc#

hypothetical protein APE0900

pir:D72685 D72685

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19812500_f1_14	993	2913	974	2925	2125	5.8e-220

Protein name Locus Name Acc#

sp:DPO1_HAEIN P43741

Description

DNA POLYMERASE I, (POL I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2008433_c1_102	994	2914	287	864		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20506502_c2_105	995	2915	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20581377_c3_127	996	2916	888	2667	2717	1.1e-282

Protein name

Locus Name

Acc#

DNA topoisomerase,

pir:G64119

G64119

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2131550_f1_9	997	2917	115	348	153	5.4e-11

Protein name

Locus Name

Acc#

pterin-4-alpha-carbinolamine
dehydratase:protein ssl2296:protein ssl2296

pir:S74881

S74881

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22119402_f3_77	998	2918	262	789	491	8.2e-47

Protein name

Locus Name

Acc#

sp:OCCM_AGRT1

P35115

Description

OCTOPINE TRANSPORT SYSTEM PERMEASE PROTEIN OCCM

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
234408_c2_l11	999	2919	129	390	275	6.3e-24

Protein name

Locus Name

Acc#

sp:RRMA_ECOLI

P36999

Description

METHYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23928130_f3_66	1000	2920	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24256553_f2_31	1001	2921	751	2256	2080	3.4e-215

Protein name

Locus Name

Acc#

DNA topoisomerase IV

gp:AB023570

AB023570

Description

Vibrio parahaemolyticus parC gene for DNA topoisomerase IV, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24645763_c1_91	1002	2922	296	891	255	8.4e-22

Protein name

Locus Name

Acc#

hypothetical protein jhp1155

pir:G71841

G71841

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24881313_f2_32	1003	2923	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25417950_c3_134	1004	2924	162	489	214	1.8e-17

Protein name

Locus Name

Acc#

sp:RRMA_ECOLI

P36999

Description

METHYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31406308_c2_113	1005	2925	114	345		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31485625_f3_72	1006	2926	275	828	427	5.0e-40

Protein name

Locus Name

Acc#

gp:AB032934

AB032934

Description

Vibrio alginolyticus pfsA, orfC, orfD genes for PF60 andhypothetical proteins, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34025462_c1_104	1007	2927	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34086012_c1_97	1008	2928	138	417		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35360075_f1_2	1009	2929	166	501	73	0.032

Protein name

nef protein

Locus Name

gp:AF169778

Acc#

AF169778

Description

HIV-1 isolate G221 from India nef protein (nef) gene, partial cds;and 3' long terminal repeat, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36110253_f2_36	1010	2930	108	327	76	0.0077

Protein name

outer surface protein A

Locus Name

gp:BBPWUDII

Acc#

X68539

Description

B.burgdorferi (PWudII) plasmid OspA gene for outer surface proteinA.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3945893_f3_71	1011	2931	286	861	825	3.3e-82

Protein name

Locus Name

gp:AB032934

Acc#

AB032934

Description

Vibrio alginolyticus pfsA, orfC, orfD genes for PF60 andhypothetical proteins, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4337963_f2_51	1012	2932	268	807	434	9.0e-41

Protein name

Locus Name

gp:AB032934

Acc#

AB032934

Description

Vibrio alginolyticus pfsA, orfC, orfD genes for PF60 andhypothetical proteins, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4691525_f1_7	1013	2933	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4735333_c2_110	1014	2934	570	1713	1749	4.0e-180

Protein name

Locus Name

Acc#

sp:RF3_HAEIN

P43928

Description

PEPTIDE CHAIN RELEASE FACTOR 3 (RF-3)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5102193_f2_54	1015	2935	372	1119	897	7.8e-90

Protein name

Locus Name

Acc#

sp:GLMU_HAEIN

P43889

Description

ACETYLGLUCOSAMINE-1-PHOSPHATE URIDYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5111013_c3_126	1016	2936	201	606		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6516518_f1_25	1017	2937	243	732	499	1.2e-47

Protein name

Locus Name

Acc#

sp:NOCQ_AGRT5

P35118

Description

NOPALINE TRANSPORT SYSTEM PERMEASE PROTEIN NOCQ

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6820875_c1_100	1018	2938	345	1038	159	8.8e-09

Protein name

Locus Name

Acc#

apolipoprotein A-IV precursor

pir:C40892

C40892

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
807692_c3_137	1019	2939	563	1692	171	1.2e-08

Protein name

Trip230

Locus Name

gp:AF007217

Acc#

AF007217

Description

Homo sapiens Trip230 mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
978502_f2_52	1020	2940	266	801	430	2.4e-40

Protein name

Locus Name

gp:AB032934

Acc#

AB032934

Description

Vibrio alginolyticus pfsA, orfC, orfD genes for PF60 andhypothetical proteins, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10056500_f1_3	1021	2941	78	237	163	4.7e-12

Protein name

hypothetical protein HI0187

Locus Name

pir:B64145

Acc#

B64145

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10656456_c3_200	1022	2942	463	1392	831	7.7e-83

Protein name

Locus Name

sp:YWBN_BACSU

Acc#

P39597

Description

HYPOTHETICAL 45.7 KD PROTEIN IN EPR-GALK INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12603450_f1_20	1023	2943	558	1677	1262	1.6e-128

Protein name

Locus Name

sp:PILB_PSEAE

Acc#

P22608

Description

FIMBRIAL ASSEMBLY PROTEIN PILB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12978955_f2_43	1024	2944	274	825	609	2.6e-59

Protein name

Locus Name

Acc#

sp:YH25_AZOCH

P54085

Description

(ORF5)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13679786_f3_112	1025	2945	110	333	105	1.2e-05

Protein name

Locus Name

Acc#

hypothetical protein

gp:BSZ75208

Z75208

Description

B.subtilis genomic sequence 89009bp.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13712643_c3_187	1026	2946	215	648	113	0.00040

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:B75483

B75483

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14191915_f2_69	1027	2947	365	1098	329	2.5e-34

Protein name

Locus Name

Acc#

conserved hypothetical protein ylbK

pir:H69874

H69874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14251568_f2_72	1028	2948	118	357	207	1.0e-16

Protein name

Locus Name

Acc#

hypothetical protein APE1486

pir:F72628

F72628

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14492180_c2_149	1029	2949	67	204		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14511561_c3_197	1030	2950	1319	3960	3473	0.0

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

phosphoribosylformylglycinamidine
synthase,:formylglycinamide ribonucleotide
synthetase:phosphoribosylformylglycinamidine

pir:SYECPG

D65033:A31

862:A34192

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14878927_f2_42	1031	2951	271	816	294	4.8e-39

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

sp:HIS2_AQUAE

O67780

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14882750_c2_164	1032	2952	409	1230	585	9.0e-57

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

putative membrane transport protein.

gp:SCC75A

AL133220

Description

Streptomyces coelicolor cosmid C75A.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
14970637_c3_176	1033	2953	237	714	791	1.3e-78

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

sp:CLPP_ECOLI

P19245

Description

PROTEIN F21.5)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15831636_c2_158	1034	2954	127	384	236	1.5e-19

Protein name

Acriflavin resistance protein D.

Locus Name

gp:D90846

Acc#

D90846:AB0
01340

Description

E.coli genomic DNA, Kohara clone #357(46.5-46.8 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
165842_c2_157	1035	2955	205	618	332	5.8e-30

Protein name

Locus Name

sp:NOLH_RHIME

Acc#

P25198

Description

NODULATION PROTEIN NOLH PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16687526_f1_10	1036	2956	448	1347	1082	1.9e-109

Protein name

Locus Name

sp:ARGA_ECOLI

Acc#

P08205:O68
009:O68010
:O68011:O6

Description

SYNTHASE) (AGS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
191675_c2_150	1037	2957	251	756	698	9.5e-69

Protein name

Locus Name

gp:AF170343

Acc#

AF170343

Description

Burkholderia cepacia 5' adenylylsulfate APS reductase (cysH) gene, complete cds; and ATP sulfurylase small subunit (cysD) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19821942_c3_205	1038	2958	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20203302_c3_185	1039	2959	226	681	141	4.0e-08

Protein name Locus Name Acc#
DnrE protein gp:PST131716 AJ131716

Description

Pseudomonas stutzeri dnrE gene and ORF235 (partial).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20570385_c2_159	1040	2960	193	582		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21494010_c2_174	1041	2961	455	1368	1377	1.1e-140

Protein name Locus Name Acc#
nitric oxide reductase gp:AF002217 AF002217

Description

Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21676712_c1_120	1042	2962	130	393	395	1.2e-36

Protein name Locus Name Acc#
sulfate adenylyltransferase subunit CysN gp:AF130466 AF130466

Description

Campylobacter jejuni peptide chain release factor 2 (prfB) gene, partial cds; alpha-2,3-sialyltransferase (cst-I) and sulfateadenylyltransferase subunit CysD (cysD) genes, complete cds; and sulfate adenylyltransferase subunit CysN (cysN) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22078812_c2_154	1043	2963	727	2184	1636	3.8e-168

Protein name

Locus Name

Acc#

sp:RECG_ECOLI

P24230:P76

Description

721

ATP-DEPENDENT DNA HELICASE RECG,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22350926_c1_115	1044	2964	724	2175	2193	3.6e-227

Protein name

Locus Name

Acc#

sp:FAOB_PSEFR

P28793

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23556252_c3_203	1045	2965	600	1803	709	6.0e-85

Protein name

Locus Name

Acc#

glutamate synthase (ferredoxin) homolog yerD

pir:C69794

C69794

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23593830_c3_199	1046	2966	340	1023	462	9.7e-44

Protein name

Locus Name

Acc#

sp:YWB_M_BACSU

P39596

Description

HYPOTHETICAL 42.8 KD PROTEIN IN EPR-GALK INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23651900_f2_48	1047	2967	328	987	634	5.8e-62

Protein name

Locus Name

Acc#

sp:YOH1_HAEIN

P44606

Description

HYPOTHETICAL PROTEIN HI0270

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
23862576_c1_124	1048	2968	153	462	182	4.5e-14

Protein name
 probable antibiotic resistance protein mtrC

Locus Name
 pir:S42418

Acc#
 S42418:S40252

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24042500_c3_183	1049	2969	313	942	608	3.3e-59

Protein name

Locus Name
 sp:CYSN_MYCTU

Acc#
 Q10600

Description
 (SULFURYLASE)

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
24302260_c3_179	1050	2970	410	1233	1331	8.0e-136

Protein name
 3-oxoacyl-CoA thiolase

Locus Name
 gp:AF150672

Acc#
 AF150672

Description
 Pseudomonas putida 3-oxoacyl-CoA thiolase (fadA) gene, completecds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25584438_c3_189	1051	2971	143	432	174	7.6e-12

Protein name
 CeoB

Locus Name
 gp:BCU97042

Acc#
 U97042

Description
 Burkholderia cepacia CeoA (ceoA) and CeoB (ceoB) genes, completecds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
25984558_c3_188	1052	2972	134	405	133	1.8e-07

Protein name
 acriflavin resistance protein D (acrD) RP170

Locus Name
 pir:F71727

Acc#
 F71727

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26741556_c1_135	1053	2973	198	597	101	0.0011

Protein name

Locus Name

Acc#

sp:HA34_BRELC

Q99074

Description

HAM34 PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3245640_c3_190	1054	2974	425	1278	265	9.4e-20

Protein name

Locus Name

Acc#

probable cation efflux system protein

pir:E71874

E71874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3375052_c1_125	1055	2975	144	435	177	3.6e-12

Protein name

Locus Name

Acc#

probable efflux transporter

pir:H71918

H71918

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34027092_c2_175	1056	2976	74	222	60	0.025

Protein name

Locus Name

Acc#

tonoplast intrinsic protein

gp:AF037061

AF037061

Description

Zea mays tonoplast intrinsic protein (ZmTIP1) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35197126_f3_79	1057	2977	179	540	155	3.3e-11

Protein name

Locus Name

Acc#

TatB protein

gp:EC05830

AJ005830

Description

Escherichia coli tatABCD operon.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35339135_f2_61	1058	2978	264	795	308	2.9e-35

Protein name

Locus Name

Acc#

sp:LEP3_AERHY

P45794

Description

TYPE 4 PREPILIN-LIKE PROTEIN SPECIFIC LEADER PEPTIDASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35395926_f1_6	1059	2979	511	1536	325	2.2e-35

Protein name

Locus Name

Acc#

probable helicase

pir:T40239

T40239

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36047308_f2_50	1060	2980	105	318		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939838_c2_173	1061	2981	66	201	189	8.2e-15

Protein name

Locus Name

Acc#

sp:RL35_PSESY

P52830

Description

50S RIBOSOMAL PROTEIN L35

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3947675_f2_46	1062	2982	250	753	375	1.6e-34

Protein name

Locus Name

Acc#

sp:HUTC_KLEAE

P12380

Description

HISTIDINE UTILIZATION REPRESSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3954218_c3_177	1063	2983	441	1326	1252	7.6e-140

Protein name

Locus Name

Acc#

sp:CLPX_HAEIN

P44838

Description

ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4328428_c1_119	1064	2984	310	933	911	2.6e-91

Protein name

Locus Name

Acc#

sp:CYSD_MYCTU

Q10599

Description

SULFURYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4485963_c3_206	1065	2985	121	366	469	1.8e-44

Protein name

Locus Name

Acc#

ribosomal protein L20

pir:R5EC20

D64930:S08
608:A02806
:I41282

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5120443_f3_94	1066	2986	214	645	363	3.0e-33

Protein name

Locus Name

Acc#

sp:YACE_VIBVU

Q56741

Description

HYPOTHETICAL 22.5 KD PROTEIN IN VVPD 3'REGION (ORFX)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5890643_f2_73	1067	2987	380	1143	131	7.7e-07

Protein name

Locus Name

Acc#

dnaJ protein homolog

pir:S34632

S34632

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
7277_f3_93	1068	2988	423	1272	664	3.8e-65

Protein name pilus assembly protein PilC Locus Name gp:AF038655 Acc# AF038655

Description

Legionella pneumophila pilus assembly protein PilB (pilB), pilus assembly protein PilC (pilC), and type IV prepilin-like proteins specific leader peptidase PilD (pild) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
978517_c2_166	1069	2989	433	1302	615	5.8e-112

Protein name Locus Name sp:GLTS_HAEIN Acc# P45240

Description

SODIUM/GLUTAMATE SYMPORT CARRIER PROTEIN (GLUTAMATE PERMEASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
10547711_c2_8	1070	2990	275	828	933	1.2e-93

Protein name Locus Name sp:ABC_HAEIN Acc# P44785

Description

ATP-BINDING PROTEIN ABC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
188807_c2_10	1071	2991	118	354	320	1.1e-28

Protein name Locus Name sp:PLPA_PASHA Acc#

Description Q08868:Q07363

OUTER MEMBRANE LIPOPROTEIN 1 PRECURSOR (PLP1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19589635_c1_7	1072	2992	99	300	190	6.5e-15

Protein name

ORF120

Locus Name

gp:ECORRNHK12

Acc#

D15061

Description

E.coli genomic DNA, 5'flanking region of rrnH gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24353193_f1_1	1073	2993	95	288	113	9.3e-07

Protein name

hypothetical protein PH0133

Locus Name

pir:C71234

Acc#

C71234

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35582056_c3_11	1074	2994	240	723	631	1.2e-61

Protein name

Locus Name

sp:YAEH_HAEIN

Acc#

P46492

Description

HYPOTHETICAL ABC TRANSPORTER PERMEASE PROTEIN HI0620.1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4144442_f2_6	1075	2995	131	396		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16924127_f1_1	1076	2996	367	1104	137	7.2e-06

Protein name

Locus Name

gp:PSENOSA

Acc#

M60717

Description

P.stutzeri NosA protein (nosA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5109792_f2_3	1077	2997	122	369		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16681688_c1_3	1078	2998	60	183	55	0.044

Protein name

Locus Name

Acc#

sp:RNH_HELPY

P56120

Description

RIBONUCLEASE H, (RNASE H)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24039143_f1_1	1079	2999	345	1038	637	2.8e-62

Protein name

Locus Name

Acc#

ornithine decarboxylase

pir:D72200

D72200

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29337840_f2_2	1080	3000	150	450	95	0.014

Protein name

Locus Name

Acc#

AvtA

gp:AF014804

AF014804

Description

Neisseria meningitidis PglB (pglB), PglC (pglC), PglD (pglD), andAvtA (avtA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11900461_f2_7	1081	3001	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14573562_f1_2	1082	3002	341	1026	1075	1.1e-108

Protein name

Locus Name

Acc#

sp:TRMU_ECOLI

Description

P25745:P75
964

(EC 2.1.1.61)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30270465_f1_3	1083	3003	249	750	185	5.7e-14

Protein name

Locus Name

Acc#

sp:YYAD_BACSU

P37520

Description

HYPOTHETICAL 37.7 KD PROTEIN IN RPSF-SPO0J INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6365936_f2_6	1084	3004	108	327	170	8.5e-13

Protein name

Locus Name

Acc#

gp:ECPURB

X59307

Description

E.coli ORF-15, ORF-23, purB and phoP (5'end) genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6537957_c1_11	1085	3005	200	603	454	6.8e-43

Protein name

Locus Name

Acc#

sp:YGBB_ECOLI

P36663

Description

HYPOTHETICAL 16.9 KD PROTEIN IN SURE-CYSC INTERGENIC REGION (ORF0)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
173187_f3_5	1086	3006	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34407827_f2_2	1087	3007	366	1101	786	4.5e-78

Protein name

Locus Name

Acc#

sp:LCFA_ECOLI

P29212

Description

SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7285152_f1_1	1088	3008	69	207		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16056563_c2_63	1089	3009	141	426	90	0.020

Protein name

Locus Name

Acc#

hypothetical wtfw protein

pir:T41252

T41252

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1986087_f3_30	1090	3010	412	1239	1316	3.1e-134

Protein name

Locus Name

Acc#

sp:SERA_HAEIN

P43885

Description

D-3-PHOSPHOGLYCERATE DEHYDROGENASE, (PGDH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2072762_f1_10	1091	3011	1220	3663	524	4.4e-93

Protein name

Locus Name

Acc#

chromosome segregation SMC
protein:minichromosome stabilizing protein
SMC

pir:G69708

G69708:JC4
819:PC4029

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21531252_f3_36	1092	3012	303	912	722	2.7e-71

Protein name

translation elongation factor EF-Ts

Locus Name

pir:EFECS

Acc#

A03525:A45

269:A32881

:S45235:B6

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23406_f1_11	1093	3013	278	837	898	6.1e-90

Protein name

Locus Name

sp:RS2_SPIPL

Acc#

P34831

Description

30S RIBOSOMAL PROTEIN S2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23437562_f1_7	1094	3014	253	762	186	3.2e-18

Protein name

hypothetical protein HP0862

Locus Name

pir:F64627

Acc#

F64627

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23613510_c2_70	1095	3015	374	1125	700	5.8e-69

Protein name

Locus Name

sp:YCFO_ECOLI

Acc#

P75949

Description

HYPOTHETICAL 37.6 KD PROTEIN IN PHUE-NDH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23861686_f3_35	1096	3016	180	543	526	1.6e-50

Protein name

invasion protein homolog

Locus Name

gp:AF116285

Acc#

AF116285

Description

Pseudomonas aeruginosa invasion protein homolog
andphosphoenolpyruvate-protein phosphotransferase PtsP (ptsP) genes, complete
cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2460181_f1_1	1097	3017	987	2964	3662	0.0

Protein name

Locus Name

Acc#

sp:RPOB_PSEPU

P19175

Description

BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25401687_c3_88	1098	3018	141	426	372	3.3e-34

Protein name

Locus Name

Acc#

gp:PAU89892

U89892

Description

Pseudomonas aeruginosa virulence factor regulator (vfr) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26064760_c3_93	1099	3019	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29890701_f3_31	1100	3020	469	1410	1678	1.3e-172

Protein name

Locus Name

Acc#

sp:GSHR_HAEIN

P43783

Description

GLUTATHIONE REDUCTASE, (GR) (GRASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32287567_f2_16	1101	3021	1422	4269	4932	0.0

Protein name

Locus Name

Acc#

99% identity over 1407 amino acids with E. coli

gp:STYSTMF1

AF170176

Description

Salmonella typhimurium fragment STMF1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907166_f1_6	1102	3022	309	930	117	1.6e-06

Protein name

putative biotin protein ligase

Locus Name

gp:AF016461

Acc#

AF016461

Description

Bordetella pertussis putative biotin protein ligase (birA) gene, complete cds and Bvg accessory factor (baf) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4507138_f1_5	1103	3023	727	2184	736	2.5e-88

Protein name

Locus Name

sp:PRC_ECOLI

Acc#

P23865

Description

PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4959501_c1_46	1104	3024	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5119452_c3_92	1105	3025	267	804	398	5.9e-37

Protein name

Locus Name

sp:Y902_HAEIN

Acc#

P44070

Description

HYPOTHETICAL PROTEIN HI0902

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11955251_c2_26	1106	3026	915	2748	2735	1.3e-284

Protein name

Locus Name

sp:SYA_ECOLI

Acc#

P00957:P78
279

Description

ALANYL-TRNA SYNTHETASE, (ALANINE--TRNA LIGASE) (ALARS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16523292_c2_25	1107	3027	488	1467	1534	2.4e-157

Protein name

Locus Name

Acc#

sp:PUR8_HAEIN

P44797

Description

ADENYLOSUCCINATE LYASE, (ADENYLOSUCCINASE) (ASL)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23475417_f3_18	1108	3028	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24308500_c1_22	1109	3029	155	468	282	1.2e-24

Protein name

Locus Name

Acc#

erythroid differentiation-related factor 2

gp:AF040248

AF040248

Description

Homo sapiens erythroid differentiation-related factor 2 mRNA,partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31444625_c3_34	1110	3030	452	1359	646	3.1e-63

Protein name

Locus Name

Acc#

sp:YCLF_BACSU

P94408

Description

HYPOTHETICAL 53.3 KD PROTEIN IN SFP-GERKA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33632752_c2_27	1111	3031	285	855	679	9.8e-67

Protein name

Locus Name

Acc#

aspartate kinase, II
precursor:lysine-sensitive aspartokinase II

pir:A48946

A48946:B48

946:C48946

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33829043_c3_33	1112	3032	106	321		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4400283_c1_23	1113	3033	95	288		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6852262_c1_21	1114	3034	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9933552_f1_3	1115	3035	82	249		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9975052_c2_24	1116	3036	132	399		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1036637_c3_276	1117	3037	61	186		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1038885_f1_26	1118	3038	416	1251	1526	1.7e-156

Protein name

lactate dehydrogenase

Locus Name

gp:NMU58911

Acc#

U58911

Description

Neisseria meningitidis lactate dehydrogenase (lldA), HI0379 homologues, complete cds, HI1054 homolog gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10547558_c1_180	1119	3039	176	531	123	8.1e-08

Protein name

hypothetical protein APE1165

Locus Name

pir:H72586

Acc#

H72586

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11711_c3_265	1120	3040	434	1305	489	1.3e-46

Protein name

HisX

Locus Name

gp:AF010189

Acc#

AF010189

Description

Pseudomonas stutzeri HflC (hflC) gene, partial cds; HisX (hisX) gene, complete cds; and PurA (purA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11991552_f3_108	1121	3041	286	861	614	7.6e-60

Protein name

Locus Name

sp:TRPC_PSEPU

Acc#

P20578

Description

INDOLE-3-GLYCEROL PHOSPHATE SYNTHASE, (IGPS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12222077_f2_53	1122	3042	198	597	469	1.8e-44

Protein name

Locus Name

sp:RECR_HAEIN

Acc#

P44712

Description

RECOMBINATION PROTEIN RECR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
136302_c1_167	1123	3043	154	465	95	0.0012

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein sll1675	pir:S74649	S74649

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13678763_c1_182	1124	3044	223	672	194	2.4e-15

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein RP471	pir:D71706	D71706

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14094452_c3_267	1125	3045	60	183		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14103402_f1_7	1126	3046	286	861	265	7.3e-23

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:YPUG_BACSU	P35154

Description

HYPOTHETICAL 29.6 KD PROTEIN IN RIBT-DACB INTERGENIC REGION (ORFX7)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14273586_f2_57	1127	3047	451	1356	1508	1.4e-154

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:ACCC_PSEAE	P37798

Description

CARBOXYLASE,) (ACC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14572132_f3_135	1128	3048	238	717	736	8.9e-73

Protein name

Locus Name

Acc#

sp:END3_HAEIN

P44319

Description

LYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14875305_f3_113	1129	3049	139	420	141	1.2e-09

Protein name

Locus Name

Acc#

Ribonuclease D (EC 3.1.13.-)

gp:D90825

D90825:AB0
01340

Description

E.coli genomic DNA, Kohara clone #334(40.6-41.0 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16507827_c3_256	1130	3050	519	1560	1030	6.3e-104

Protein name

Locus Name

Acc#

sp:NADB_PSEAE

Q51363:Q51
412

Description

L-ASPARTATE OXIDASE, (QUINOLINATE SYNTHETASE B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16510254_c1_154	1131	3051	308	927	1063	2.0e-107

Protein name

Locus Name

Acc#

sp:RF1_ECOLI

P07011:P77
340

Description

PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16829177_c1_172	1132	3052	95	288	83	0.041

Protein name

Locus Name

Acc#

FIN21.17

gp:AC002130

AC002130

Description

The sequence of BAC FIN21 from Arabidopsis thaliana chromosome 1, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19562800_f2_52	1133	3053	120	363	273	1.0e-23

Protein name

Locus Name

Acc#

sp:YBAB_HAEIN

P44711

Description

HYPOTHETICAL PROTEIN HI0442

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20312551_f1_8	1134	3054	202	609	243	1.6e-20

Protein name

Locus Name

Acc#

sp:YPUH_BACSU

P35155

Description

HYPOTHETICAL 22.0 KD PROTEIN IN RIBT-DACB INTERGENIC REGION (ORFX8)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20573252_c2_229	1135	3055	205	618	309	1.6e-27

Protein name

Locus Name

Acc#

sp:YDJA_ECOLI

P24250

Description

HYPOTHETICAL 20.1 KD PROTEIN IN SELD-SPPA INTERGENIC REGION (ORF183)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21667027_f2_89	1136	3056	832	2499	2093	1.4e-216

Protein name

Locus Name

Acc#

sp:LON_ERWAM

P46067

Description

ATP-DEPENDENT PROTEASE LA,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21681503_f1_9	1137	3057	329	990	758	4.2e-75

Protein name

Locus Name

Acc#

sp:YCIL_HAEIN

P45104

Description

HYPOTHETICAL PROTEIN HI1199

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21754681_f3_119	1138	3058	197	594	284	7.1e-25

Protein name

Locus Name

Acc#

sp:YBEY_ECOLI

P77385

Description

HYPOTHETICAL 17.5 KD PROTEIN IN CUTE-ASNB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22128380_f1_41	1139	3059	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22384635_f1_31	1140	3060	190	573	604	8.7e-59

Protein name

Locus Name

Acc#

HemO

gp:AF133695

AF133695

Description

Neisseria meningitidis HemO (hemO) gene, complete cds; and HmbR(hmbR) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23444377_c1_199	1141	3061	492	1479	2364	2.7e-245

Protein name

Locus Name

Acc#

outer membrane protein E

gp:MBOOMPE

L31788

Description

Moraxella catarrhalis outer membrane protein E gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
234700_c3_268	1142	3062	344	1035	1002	5.8e-101

Protein name

Locus Name

Acc#

unknown

gp:AF109131

AF109131

Description

Sinorhizobium meliloti homogentisate dioxygenase (hmgA) and maleylacetoacetate isomerase (maiA) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23620263_c3_271	1143	3063	267	804	534	2.3e-51

Protein name

Locus Name

Acc#

sp:KDSB_ECOLI

P04951

Description

SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23651513_f1_43	1144	3064	259	780	589	3.4e-57

Protein name

Locus Name

Acc#

sp:NADC_RHORU

P77938

Description

) (QAPRTASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24031586_f1_5	1145	3065	383	1152	976	3.3e-98

Protein name

Locus Name

Acc#

sp:TRPD_ACICA

P00500

Description

ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24397555_f3_140	1146	3066	219	660	165	1.2e-11

Protein name

Locus Name

Acc#

probable corA protein

pir:F70952

F70952

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415782_f3_106	1147	3067	61	186	87	0.0079

Protein name

Locus Name

Acc#

UUP protein

gp:ECUUP

Y09439

Description

E.coli uup gene, partial.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24721962_c3_282	1148	3068	77	234		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24801937_c2_236	1149	3069	63	192		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26756325_f1_1	1150	3070	314	945	1021	5.6e-103

Protein name Locus Name Acc#

sp:OTCA_PSESH Q02047

Description

(EC 2.1.3.3) (OTCASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26757790_c3_255	1151	3071	376	1131	1065	1.2e-107

Protein name Locus Name Acc#

sp:NADA_ECOLI

P11458:P77
373

Description

QUINOLINATE SYNTHETASE A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2742036_f1_3	1152	3072	144	435	426	6.3e-40

Protein name Locus Name Acc#

sp:PAND_BACSU

P52999

Description

DECARBOXYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29301691_f1_14	1153	3073	248	747	140	4.7e-07

Protein name

Locus Name

Acc#

sp:RND_HAEIN

P44442

Description

RIBONUCLEASE D, (RNASE D)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29355287_f2_99	1154	3074	74	225	79	0.013

Protein name

Locus Name

Acc#

MutT/nudix family protein

pir:A75550

A75550

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29484626_c1_173	1155	3075	356	1071	555	2.4e-57

Protein name

Locus Name

Acc#

sp:YGI2_PSEPU

P31857

Description

HYPOTHETICAL 32.4 KD PROTEIN IN GIDB-UNCI INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29531392_f1_40	1156	3076	124	375	173	1.5e-11

Protein name

Locus Name

Acc#

lustrin A

pir:T08852

T08852

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29572155_f2_49	1157	3077	343	1032	406	8.3e-38

Protein name

Locus Name

Acc#

sp:HTRB_HAEIN

P45239:Q48
045

Description

PROTEIN B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29890631_f2_56	1158	3078	157	474	259	3.1e-22

Protein name

Locus Name

Acc#

sp:BCCP_HAEIN

P43874

Description

BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE (BCCP)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30204837_c2_230	1159	3079	447	1344	628	2.5e-61

Protein name

Locus Name

Acc#

sp:GPDA_ECOLI

P37606

Description

,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30330056_f2_48	1160	3080	233	702	506	2.1e-48

Protein name

Locus Name

Acc#

putative ATP-binding protein

gp:NME242841

AJ242841

Description

Neisseria meningitidis DNA for opcA region, strain Z2491.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32878_c2_250	1161	3081	80	243	89	0.00033

Protein name

Locus Name

Acc#

sp:SLYX_ECOLI

P30857

Description

SLYX PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34180317_f1_22	1162	3082	115	348	420	2.7e-39

Protein name

Locus Name

Acc#

sp:YCHF_HAEIN

P44681

Description

PROBABLE GTP-BINDING PROTEIN HI0393

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34417090_f3_151	1163	3083	76	231		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35196902_f3_129	1164	3084	616	1851	631	1.2e-61

Protein name Locus Name Acc#

L-lactate permease (lctP) homolog pir:F69350 F69350

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35335137_c1_175	1165	3085	330	993	302	8.7e-27

Protein name Locus Name Acc#

sp:HOLB_PSEAE P52024

Description

DNA POLYMERASE III, DELTA' SUBUNIT,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35353443_c2_215	1166	3086	347	1044	1128	2.6e-114

Protein name Locus Name Acc#

sp:PURA_VIBPA P40607

Description

ADENYLOSUCCINATE SYNTHETASE, (IMP--ASPARTATE LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35603128_f3_150	1167	3087	80	243		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3914143_c2_209	1168	3088	185	558	256	2.1e-29

Protein name

ExbB protein

Locus Name

gp:BPE132741

Acc#

AJ132741

Description

Bordetella pertussis hupB, tonB, exbB, exbD and basR genes and ORF1 (partial).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3914811_c3_280	1169	3089	370	1113	873	2.7e-87

Protein name

Locus Name

sp:YHCM_ECOLI

Acc#

P46442

Description

HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3937518_c1_171	1170	3090	264	795	618	2.9e-60

Protein name

Locus Name

sp:YGI1_PSEPU

Acc#

P31856

Description

HYPOTHETICAL 28.9 KD PROTEIN IN GIDB-UNCI INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3938818_c1_166	1171	3091	65	198	228	6.1e-19

Protein name

PurA

Locus Name

gp:AF010189

Acc#

AF010189

Description

Pseudomonas stutzeri HfIC (hfIC) gene, partial cds; HisX (hisX) gene, complete cds; and PurA (purA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3946931_f3_114	1172	3092	216	651	560	4.0e-54

Protein name

Locus Name

gp:ECU89166

Acc#

U89166

Description

Eikenella corrodens lysine decarboxylase (ECORLD) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3960260_f1_23	1173	3093	253	762	282	1.2e-24

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable transcription regulator	pir:T34763	T34763

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4022217_f2_68	1174	3094	160	483	86	0.00087

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein F53A9.8	pir:T16439	T16439

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4023443_c3_278	1175	3095	146	441	498	1.5e-47

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:NDK_PSEAE	Q59636

Description

NUCLEOSIDE DIPHOSPHATE KINASE, (NDK) (NDP KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4101387_f1_4	1176	3096	219	660	710	5.1e-70

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:TRPG_PSEAE	P20576

Description

TRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4145000_f2_47	1177	3097	415	1248	962	1.0e-96

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:UUP1_HAEIN	

Description Q57242:005056

ABC TRANSPORTER ATP-BINDING PROTEIN UUP-1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4181502_f3_149	1178	3098	130	393		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4182762_f2_51	1179	3099	358	1077	374	1.9e-49

Protein name Locus Name Acc#

tryptophan--tRNA ligase, pir:H70385 H70385

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
424203_f1_24	1180	3100	350	1053	542	3.2e-52

Protein name Locus Name Acc#

putative exodeoxyribonuclease (EC 3.1.11.2). gp:SCE87 AL132674

Description

Streptomyces coelicolor cosmid E87.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4331262_f3_141	1181	3101	222	669	402	2.2e-37

Protein name Locus Name Acc#

probable corA protein pir:F70952 F70952

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4506930_c1_174	1182	3102	356	1071	504	3.4e-48

Protein name Locus Name Acc#

sp:LPXK_HAEIN P44491

Description

TETRAACYLDISACCHARIDE 4'-KINASE, (LIPID A 4'-KINASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4537837_f3_145	1183	3103	216	651	477	2.5e-45

Protein name

YciB homolog

Locus Name

gp:AF114793

Acc#

AF114793

Description

Vitreoscilla sp. YciB homolog, putative transcriptional activator, putative outer membrane protein, BioA homolog, and glutaminyl synthetase homolog genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4571880_f1_16	1184	3104	216	651	437	4.3e-41

Protein name

YbeZ protein

Locus Name

gp:STY249116

Acc#

AJ249116

Description

Salmonella typhimurium yleB (partial), miaB, ybeZ and ybeY(partial) genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4722125_c2_211	1185	3105	465	1398	1197	1.3e-121

Protein name

Locus Name

sp:Y325_HAEIN

Acc#

P44640

Description

HYPOTHETICAL PROTEIN HI0325

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4798763_c1_155	1186	3106	141	426	274	8.1e-24

Protein name

ExbD protein

Locus Name

gp:BPE132741

Acc#

AJ132741

Description

Bordetella pertussis hupB, tonB, exbB, exbD and basR genes and ORF1(partial).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4876005_f1_30	1187	3107	828	2487	1231	3.1e-125

Protein name

hypothetical protein TM1869

Locus Name

pir:F72202

Acc#

F72202

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4978375_c3_293	1188	3108	382	1149	261	7.7e-26

Protein name

beta-ketoacyl-acyl carrier protein synthase
III

Locus Name

pir:B64545

Acc#

B64545

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5194068_f1_35	1189	3109	620	1863	1268	3.8e-129

Protein name

Locus Name

sp:KEFX_HAEIN

Acc#

P44933

Description

ANTIPORTER)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5976555_f3_111	1190	3110	769	2310	3096	0.0

Protein name

Locus Name

sp:RIR1_ECOLI

Acc#

P00452:P78
088:P78177

Description

(RIBONUCLEOTIDE REDUCTASE 1) (B1 PROTEIN) (R1 PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
636513_f3_126	1191	3111	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6516_f2_45	1192	3112	361	1086	176	7.2e-13

Protein name

hypothetical protein

Locus Name

pir:S76259

Acc#

S76259

Description

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
phosphoglycerate mutase	pir:G72260	G72260

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6837827_c1_183	1194	3114	165	498	145	3.8e-10

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:Y400 SYNY3	Q55129

HYPOTHETICAL 18.3 KD PROTEIN SLL0400

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF114793	AF114793

Vitreoscilla sp. YciB homolog, putative transcriptional activator, putative outer membrane protein, BioA homolog, and glutamine synthetase homolog genes, complete cds; and unknown genes.

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:GIDB ECOLI	P17113

GLUCOSE INHIBITED DIVISION PROTEIN B

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
probable GTP-binding protein HI0393	pir:164150	I64150

320

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
976531_f2_59	1198	3118	171	516	437	4.3e-41

Protein name YbeZ protein Locus Name gp:STY249116 Acc# AJ249116

Description

Salmonella typhimurium yleB (partial), miaB, ybeZ and ybeY(partial) genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
985925_f3_124	1199	3119	128	387		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9954828_c2_208	1200	3120	322	969	170	3.9e-14

Protein name TonB2 Locus Name gp:AF190125 Acc# AF190125

Description

Pseudomonas aeruginosa TonB2 (tonB2), ExbB (exbB), and ExbD (exbD) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10975667_c2_74	1201	3121	376	1131	524	2.6e-50

Protein name thiamine-monophosphate kinase Locus Name gp:D17333 Acc# D17333

Description

E. Coli thiL gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12500081_c3_90	1202	3122	270	813	855	2.2e-85

Protein name Locus Name sp:HIS6_AZOBR Acc# P26721

Description

HISF PROTEIN (CYCLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14572127_c1_50	1203	3123	165	498	433	1.1e-40

Protein name

Locus Name

Acc#

sp:RISB_ECOLI

Description

P25540:P77
114

(LUMAZINE SYNTHASE) (RIBOFLAVIN SYNTHASE BETA CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
197212_c1_54	1204	3124	284	852		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21767011_f3_32	1205	3125	317	954	736	8.9e-73

Protein name

Locus Name

Acc#

YafJ

gp:NGAJ2783

AJ002783

Description

Neisseria gonorrhoeae aroK, aroB, yafJ genes and open readingframe.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23645263_c3_93	1206	3126	201	606	190	2.4e-30

Protein name

Locus Name

Acc#

sp:PGPA_HAEIN

P44157

Description

PHOSPHATIDYLGLYCEROPHOSPHATASE A,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23916007_c3_94	1207	3127	196	591	273	1.0e-23

Protein name

Locus Name

Acc#

methylase

gp:LLCPJW565

Y12736

Description

Lactococcus lactis cremoris plasmid pJW565 DNA, abiIM, abiIR genesand orfX.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23947167_f3_37	1208	3128	653	1962	756	6.0e-87

Protein name

penicillin-binding protein 3

Locus Name

pir:S54872

Acc#

S54872

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24256687_f2_23	1209	3129	501	1506	537	1.8e-79

Protein name

Locus Name

sp:MURF_ECOLI

Acc#

P11880:P77
636:007100

Description

(D-ALANYL-D-ALANINE-ADDING ENZYME)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24353377_c1_45	1210	3130	225	678	155	3.3e-11

Protein name

hypothetical protein PAB0131

Locus Name

pir:D75209

Acc#

D75209

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26369016_f2_18	1211	3131	299	900		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3397336_c1_49	1212	3132	65	198	50	0.037

Protein name

Locus Name

sp:DHSD_FORPU

Acc#

P80479

Description

DEHYDROGENASE, SUBUNIT IV)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35968792_f2_24	1213	3133	201	606	346	1.9e-31

Protein name

Locus Name

Acc#

sp:TPIS_MORSP

Q01893

Description

TRIOSEPHOSPHATE ISOMERASE, (TIM)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3907500_f1_5	1214	3134	341	1026	227	9.2e-18

Protein name

Locus Name

Acc#

homoserine kinase homolog

pir:T33726

T33726

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939665_c1_51	1215	3135	183	552	204	2.1e-16

Protein name

Locus Name

Acc#

sp:NUSB_HAETN

P45150

Description

N UTILIZATION SUBSTANCE PROTEIN B HOMOLOG (NUSB PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3953191_c1_44	1216	3136	502	1509	1501	7.7e-154

Protein name

Locus Name

Acc#

glutamyl-tRNA synthetase

gp:AF139107

AF139107

Description

Pseudomonas aeruginosa hypothetical multidrug resistance protein(mdr) gene, partial cds; hypothetical transcriptional activator(act) and glutamyl-tRNA synthetase (gltX) genes, complete cds; andtRNA-Ala and tRNA-Glu genes, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
41703_f3_36	1217	3137	120	363		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4301943_f1_13	1218	3138	368	1107	1018	1.2e-102

Protein name

Locus Name

Acc#

sp:MRAY_HAEIN

P45062

Description

(UDP-MURNAC-PENTAPEPTIDE PHOSPHOTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5111318_f2_22	1219	3139	523	1572	756	6.8e-75

Protein name

Locus Name

Acc#

probable

gp:AF141867

AF141867

Description

Vibrio cholerae
probableUDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate
ligase(murE) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6754052_f3_35	1220	3140	336	1011	695	2.0e-68

Protein name

Locus Name

Acc#

sp:YABC_ECOLI

P18595

Description

HYPOTHETICAL 34.9 KD PROTEIN IN FRUR-FTSL INTERGENIC REGION (ORFB)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
111552_f1_10	1221	3141	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1189035_c3_48	1222	3142	179	540	616	4.7e-60

Protein name

Locus Name

Acc#

adenylate kinase

gp:AB024426

AB024426

Description

Pseudomonas putida adk gene for adenylate kinase, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12578208_f2_15	1223	3143	386	1161	1244	1.3e-126

Protein name

Locus Name

Acc#

sp:DHAS_PSEAE

Q51344

Description

DEHYDROGENASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23444507_c3_45	1224	3144	452	1359		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23536511_f2_16	1225	3145	338	1017	210	4.1e-15

Protein name

Locus Name

Acc#

sp:ASG1_ECOLI

P18840

Description

(L-ASNASE I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
245682_f1_8	1226	3146	303	912	689	8.5e-68

Protein name

Locus Name

Acc#

sp:TRUA_ECOLI

P07649

Description

I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE) (PSU-I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34157662_c2_41	1227	3147	203	612	321	8.5e-29

Protein name

Locus Name

Acc#

sp:TIPB_PSEFL

P52237

Description

BIOGENESIS PROTEIN TIPB)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4042131_c1_33	1228	3148	70	213		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4112793_c1_37	1229	3149	423	1272	175	3.1e-10

Protein name Locus Name Acc#

sp:CCMH_HAEIN P46458

Description

CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCMH PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4484436_c2_40	1230	3150	692	2079	1743	1.7e-179

Protein name Locus Name Acc#

sp:CCMF_PSEFL P52225

Description

CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5265800_f1_9	1231	3151	77	234	274	8.1e-24

Protein name Locus Name Acc#

sp:IF1_BACSU P20458

Description

TRANSLATION INITIATION FACTOR IF-1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
587775_c1_36	1232	3152	172	519	299	1.8e-26

Protein name Locus Name Acc#

sp:CCMH_ECOLI P33925

Description

CYTOCHROME C-TYPE BIOGENESIS PROTEIN CCMH PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5894082_f1_7	1233	3153	206	621	309	1.6e-27

Protein name

Locus Name

Acc#

sp:YHHF_ECOLI

P10120

Description

21.7 KD PROTEIN IN FTSY-NIKA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1058462_c3_105	1234	3154	283	852	77	0.032

Protein name

Locus Name

Acc#

15 kDa vesicular-like antigen

gp:PFAVLAP

M94732

Description

Plasmodium falciparum 15 kDa vesicular-like antigen gene, exons 1through 4.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13688802_c2_101	1235	3155	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14644586_f2_28	1236	3156	391	1176	465	4.7e-44

Protein name

Locus Name

Acc#

36 kDa protein

gp:HPU86610

U86610

Description

Helicobacter pylori 36 kDa protein gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16132787_f3_50	1237	3157	105	318	197	1.2e-15

Protein name

Locus Name

Acc#

sp:YDCQ_ECOLI

P76107

Description

HYPOTHETICAL 16.1 KD PROTEIN IN TEHB-ANSP INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
19532661_f2_33	1238	3158	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20335427_c2_78	1239	3159	657	1974	239	2.0e-17

Protein name

Locus Name

Acc#

minor tail protein gp26-related protein

pir:F75605

F75605

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21642510_c2_77	1240	3160	69	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
21909377_f2_29	1241	3161	401	1206	261	3.0e-21

Protein name

Locus Name

Acc#

hypothetical protein jhp1380

pir:G71815

G71815

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
22266577_f2_21	1242	3162	220	663	233	1.8e-19

Protein name

Locus Name

Acc#

thiamine-phosphate pyrophosphorylase

gp:AF180145

AF180145

Description

Zymomonas mobilis GTP-binding protein CgpA (cgpA), 60KDinner-membrane protein yidC (yidC), hypothetical protein, glutamine-pyruvate aminotransferase gltB (gltB), glutamate synthase small subunit gltS (gltS), undecaprenol kinase udk (udk), hypothetical protein, NADH dehydrogenase, hypothetical protein; zml2orf5, hypothetical protein, aspartate aminotransferase A, beta-hydroxysteroid dehydrogenase, phosphomannomutase pmm

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22894061_c3_119	1243	3163	165	498	222	2.6e-18

Protein name

Locus Name

Acc#

sp:TOLR_PSEAE

P50599

Description

TOLR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23444426_f3_45	1244	3164	419	1260	642	8.3e-94

Protein name

Locus Name

Acc#

ATP-dependent helicase HrpA homolog.

gp:D90779

D90779:D90
761:AB0013
40

Description

E.coli genomic DNA, Kohara clone #268(31.6-32.0 min.).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24021016_f3_43	1245	3165	1195	3588	2225	1.6e-266

Protein name

Locus Name

Acc#

sp:MFD_HAEIN

P45128

Description

TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24401887_c1_62	1246	3166	114	345	165	2.9e-12

Protein name

Locus Name

Acc#

gp:AB030825

AB030825

Description

Pseudomonas aeruginosa genomic DNA, partial sequence, strain:PA01.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25554561_f2_20	1247	3167	151	456	94	0.0015

Protein name

Locus Name

Acc#

hypothetical protein PH1001

pir:D71092

D71092

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2994032_c2_82	1248	3168	264	795	307	9.6e-35

Protein name

minor tail protein gp19

Locus Name

pir:T13105

Acc#

T13105

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31916632_f1_8	1249	3169	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3320327_c2_76	1250	3170	94	285		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34188892_c1_61	1251	3171	673	2022	227	4.5e-15

Protein name

Locus Name

Acc#

sp:VG26_BPMD2

064220

Description

MINOR TAIL PROTEIN GP26

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34415711_f1_10	1252	3172	368	1107	288	2.7e-25

Protein name

Locus Name

Acc#

conserved hypothetical integral membrane protein HP1486

pir:F64705

F64705

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35367058_f3_51	1253	3173	76	231	151	8.8e-11

Protein name

Locus Name

Acc#

sp:YDCQ_ECOLI

P76107

Description

HYPOTHETICAL 16.1 KD PROTEIN IN TEHB-ANSP INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35942905_f2_19	1254	3174	156	471	278	3.1e-24

Protein name

Locus Name

Acc#

sp:YIBK_ECOLI

P33899

Description

HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE YIBK,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36118750_c2_104	1255	3175	77	234		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36328956_f2_23	1256	3176	108	327		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3944450_c2_93	1257	3177	232	699	422	1.7e-39

Protein name

Locus Name

Acc#

TolQ protein

gp:PPPAL1

X74218

Description

Pseudomonas putida ruvB, tolQ, tolR, tolA, tolB and oprL genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4460387_f1_9	1258	3178	514	1545	240	3.4e-17

Protein name

hypothetical protein jhp1382

Locus Name

pir:A71816

Acc#

A71816

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4507703_c2_103	1259	3179	102	309	157	2.0e-11

Protein name

Locus Name

sp:Y014_BPHP1

Acc#

P51716

Description

HYPOTHETICAL 14.9 KD PROTEIN IN REP-HOL INTERGENIC REGION (ORF14)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4728415_c3_120	1260	3180	276	831	103	0.030

Protein name

ras interacting protein RIPA

Locus Name

gp:AF159241

Acc#

AF159241

Description

Dictyostelium discoideum ras interacting protein RIPA (ripA) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4730050_c1_73	1261	3181	439	1320	375	1.6e-34

Protein name

TolB

Locus Name

gp:HIU32470

Acc#

U32470

Description

Haemophilus influenzae tolQRAB gene cluster, inner membrane protein(tolQ) gene, partial cds, inner membrane protein (tolR), outer membrane integrity protein (tolA) and colicin tolerance protein(tolB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5282805_c1_63	1262	3182	227	684	329	1.2e-29

Protein name

minor tail protein L homolog:protein gp18

Locus Name

pir:T13104

Acc#

T13104

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5348393_c2_83	1263	3183	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
682777_c2_79	1264	3184	139	420		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7265950_f1_7	1265	3185	1014	3045	726	3.1e-134

Protein name

Locus Name

Acc#

sp:HRPA_ECOLI

Description

P43329:P77
479:P76861
:P76863

ATP-DEPENDENT HELICASE HRPA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24113927_f2_1	1266	3186	334	1005	116	0.0012

Protein name

Locus Name

Acc#

STARP antigen

gp:PRSTARPA

Z30339

Description

P.reichenowi STARP gene for STARP antigen.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25673906_f1_1	1267	3187	206	621	435	7.0e-41

Protein name

Locus Name

Acc#

sp:YYCF_BACSU

P37478

Description

INTERGENIC REGION

Protein name	Locus Name	Acc#
probable two component sensor protein	pir:C70624	C70624

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35210305_f1_2	1269	3189	300	903	155	2.3e-08

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
SmeS	gp:AF173226	AF173226

Stenotrophomonas maltophilia multidrug efflux system SmeR (smeR), SmeS (smeS), SmeA (smeA), SmeB (smeB), and SmeC (smeC) genes, complete cds.

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
	sp:PAL PSEPU	P43036

PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN PRECURSOR

Protein name	Locus Name	Acc#
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NO-HIT

Protein name	Locus Name	Acc#
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NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14875327_f2_18	1273	3193	867	2604	1592	1.7e-163

Protein name

membrane alanyl aminopeptidase

Locus Name

gp:AF157493

Acc#

AF157493

Description

Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
156258_c3_90	1274	3194	199	600	126	2.6e-06

Protein name

NrpG

Locus Name

gp:PMU46488

Acc#

U46488

Description

Proteus mirabilis NrpS (nrpS) gene, partial cds, NrpU (nrpU), NrpT (nrpT), NrpA (nrpA), NrpB (nrpB), NrpG (nrpG) and IrpP (irpP) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16180387_f3_36	1275	3195	384	1155	143	3.8e-07

Protein name

hypothetical protein RP367

Locus Name

pir:H71693

Acc#

H71693

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16507676_c2_64	1276	3196	338	1017	445	6.1e-42

Protein name

Locus Name

sp:SMTA_ECOLI

Acc#

P36566:P77
586

Description

SMTA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22116326_f2_14	1277	3197	109	330	205	1.7e-16

Protein name

Locus Name

sp:PA1_KLEPN

Acc#

P37446

Description

ACYLHYDROLASE) (OUTER MEMBRANE PHOSPHOLIPASE A) (OM PLA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22694056_f1_11	1278	3198	637	1914	1865	2.1e-192

Protein name

Locus Name

Acc#

sp:CLPB_HAEIN

P44403

Description

CLPB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23495633_f2_15	1279	3199	349	1050	105	0.0072

Protein name

Locus Name

Acc#

ComB

gp:AF027189

AF027189

Description

Acinetobacter sp. BD413 lytB, comB, comC, comE, and comF genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2376890_c2_56	1280	3200	90	273		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24395640_f3_38	1281	3201	282	849	291	1.3e-25

Protein name

Locus Name

Acc#

ABC transporter potG

pir:B71694

B71694

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24643831_f1_3	1282	3202	346	1041	213	3.2e-16

Protein name

Locus Name

Acc#

phospholipase A

gp:CCPLDA

Y11031

Description

C.coli pldA gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24783453_f2_25	1283	3203	224	675	738	5.5e-73

Protein name

Locus Name

Acc#

sp:CLPB_BACNO

P17422

Description

CLPB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25817157_f3_34	1284	3204	250	753	319	1.4e-28

Protein name

Locus Name

Acc#

hypothetical protein

gp:AHWAAA179

Z96927

Description

Acinetobacter haemolyticus waaA gene, strain ATCC 17906.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2995252_f3_37	1285	3205	342	1029	198	1.4e-13

Protein name

Locus Name

Acc#

ct391 hypothetical protein

pir:G72072

G72072

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32703126_f2_22	1286	3206	304	915	369	6.9e-34

Protein name

Locus Name

Acc#

hypothetical protein RP368

pir:A71694

A71694

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35368941_f1_4	1287	3207	285	858	152	4.5e-09

Protein name

Locus Name

Acc#

competence protein ComF

gp:PST249742

AJ249742

Description

Pseudomonas stutzeri JM300 bioB (partial), comF and dof (partial) genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35943885_c2_66	1288	3208	413	1242		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4111633_f2_13	1289	3209	154	465		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4142186_f1_2	1290	3210	246	741	777	4.0e-77

Protein name

Locus Name

Acc#

sp:RNPH_PSEAE

P50597

Description

NUCLEOTIDYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4572203_f1_9	1291	3211	329	990	117	5.7e-05

Protein name

Locus Name

Acc#

merozoite surface antigen 2

gp:U91655

U91655

Description

Plasmodium falciparum isolate V310, merozoite surface antigen 2 (MSP-2) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4797282_c2_74	1292	3212	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5082637_f3_33	1293	3213	440	1323	635	4.5e-62

Protein name

WaaA

Locus Name

gp:AF026386

Acc#

AF026386

Description

Salmonella typhimurium strain LT2 LPS core oligosaccharidebiosynthesis region, WaaY (waaY) gene, partial cds; WaaJ (waaJ), WaaI (waaI), WaaB (waaB), WaaP (waaP), WaaG (waaG), and WaaQ (waaQ) genes, complete cds; and WaaA (waaA) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5132838_f1_5	1294	3214	255	768		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5867075_f3_29	1295	3215	202	609	105	0.00049

Protein name

pilV protein

Locus Name

pir:S77594

Acc#

S77594

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
790700_c2_65	1296	3216	379	1140	151	9.2e-08

Protein name

hypothetical protein TP0565

Locus Name

pir:C71308

Acc#

C71308

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9775283_c1_46	1297	3217	499	1500	469	1.8e-44

Protein name

probable alginate O-acetylation protein (algI)

Locus Name

pir:D71308

Acc#

D71308

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
115827_c1_7	1298	3218	330	993	877	1.0e-87

Protein name

Locus Name

Acc#

sp:GLMU_HAEIN

P43889

Description

ACETYLGLUCOSAMINE-1-PHOSPHATE URIDYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16828178_f1_2	1299	3219	616	1851	2166	2.6e-224

Protein name

Locus Name

Acc#

sp:TYPA_HAEIN

P44910

Description

GTP-BINDING PROTEIN TYPA/BIPA HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32656465_c2_10	1300	3220	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3336053_f1_1	1301	3221	133	402	618	2.9e-60

Protein name

Locus Name

Acc#

outer membrane protein CD precursor

pir:S39866

S39866

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10975831_c3_12	1302	3222	92	279		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15912757_c1_8	1303	3223	123	372	86	0.048

Protein name

FIP2

Locus Name

gp:AF061034

Acc#

AF061034

Description

Homo sapiens FIP2 alternatively translated mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22457187_f3_5	1304	3224	250	753	888	7.0e-89

Protein name

Locus Name

sp:Y882_HAEIN

Acc#

P44068

Description

HYPOTHETICAL PROTEIN HI0882

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35271883_f1_4	1305	3225	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22848457_f2_3	1306	3226	134	405		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22853376_f3_5	1307	3227	239	720		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29296968_c3_9	1308	3228	77	234		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
976678_c3_10	1309	3229	190	570	265	7.3e-23

Protein name Locus Name Acc#

sp:PRTR_PSEAE Q06553

Description

TRANSCRIPTION REGULATORY PROTEIN PRTR (PYOSIN REPRESSOR PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
989077_f1_1	1310	3230	122	369		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1062575_c3_34	1311	3231	109	330		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11125280_f3_13	1312	3232	146	441	538	8.6e-52

Protein name Locus Name Acc#

nifU protein homolog H10377 pir:C64064 C64064

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1297092_c1_20	1313	3233	111	336	174	3.9e-12

Protein name

probable gamma-glutamyltranspeptidase precursor

Locus Name

pir:E70682

Acc#

E70682

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15892918_c3_35	1314	3234	110	333	222	2.4e-17

Protein name

probable gamma-glutamyltranspeptidase

Locus Name

pir:T34901

Acc#

T34901

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20727194_c2_24	1315	3235	91	276	318	1.8e-28

Protein name

Locus Name

gp:AF017750

Acc#

AF017750

Description

Haemophilus ducreyi cytochrome C-type biogenesis protein (ccmH), recombinational DNA repair protein (recR), manganese superoxidizedismutase (sodA), and CitG protein homolog (citG) genes, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21679025_f1_1	1316	3236	420	1263	1516	2.0e-155

Protein name

Locus Name

sp:NIFS_ECOLI

Acc#

P39171:P76
581:P76992

Description

NIFS PROTEIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31797152_f3_14	1317	3237	186	561	224	1.6e-18

Protein name

Locus Name

sp:HSCB_ECOLI

Acc#

P36540

Description

CHAPERONE PROTEIN HSCB (HSC20)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32244203_c2_26	1318	3238	72	219	125	5.0e-08

Protein name

Locus Name

Acc#

sp:VCH231122

AJ231122

Description

Vibrio cholerae z61f gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33398287_f2_5	1319	3239	178	537	396	9.6e-37

Protein name

Locus Name

Acc#

sp:YFHP_HAEIN

P44675

Description

HYPOTHETICAL PROTEIN HI0379

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36129678_f1_2	1320	3240	112	339	384	1.8e-35

Protein name

Locus Name

Acc#

sp:YFHF_HAEIN

P44672

Description

HYPOTHETICAL PROTEIN HI0376

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36220382_c2_25	1321	3241	120	363	174	3.2e-12

Protein name

Locus Name

Acc#

sp:GGT_PIG

P20735

Description

GLUTAMYLTRANSFERASE) (GGT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4331938_f2_9	1322	3242	622	1869	1435	7.6e-147

Protein name

Locus Name

Acc#

sp:HSCA_HAEIN

P44669

Description

CHAPERONE PROTEIN HSCA (HSC66)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4332838_f2_10	1323	3243	115	348	397	7.5e-37

Protein name

ferredoxin

Locus Name

gp:AF096864

Acc#

AF096864

Description

Pseudomonas aeruginosa heat shock protein (hscB), heat shockprotein 66-KDa (hscA), ferredoxin (fdx), and nucleoside diphosphatekinase (ndk) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5898593_c2_28	1324	3244	119	360		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7070215_c2_27	1325	3245	161	486	351	5.6e-32

Protein name

putative gamma-glutamyltranspeptidase precursor

Locus Name

gp:PST249741

Acc#

AJ249741

Description

Pseudomonas stutzeri JM300 gacS (partial) and ggtB (partial) genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12915808_f3_10	1326	3246	200	603		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20737503_f3_8	1327	3247	371	1116	418	4.5e-39

Protein name

probable permease perM homolog (perM) RP630

Locus Name

pir:E71668

Acc#

E71668

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22000293_c2_13	1328	3248	97	294	348	1.2e-31

Protein name

50S ribosomal protein homolog

Locus Name

gp:AF153712

Acc#

AF153712

Description

Pseudomonas sp. BG33R strain BG33R 50S ribosomal protein homologene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23863307_f3_9	1329	3249	261	786	194	2.4e-15

Protein name

Locus Name

sp:YFGE_HAEIN

Acc#

O86235

Description

HYPOTHETICAL PROTEIN H11225.1

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24308561_c3_17	1330	3250	182	549	710	5.1e-70

Protein name

phosphoribosylformylglycinamide
cyclo-ligase, :5'-phosphoribosyl-5-aminoimidazole
synthetase

Locus Name

pir:AJECPC

Acc#

A25955:B65
026

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26277251_c3_18	1331	3251	131	396	352	4.4e-32

Protein name

Locus Name

sp:PUR5_ECOLI

Acc#

P08178

Description

(PHOSPHORIBOSYL-AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6142915_c2_14	1332	3252	228	687	382	2.9e-35

Protein name

5'-phosphoribosylglycinamide transformylase

Locus Name

gp:STU68765

Acc#

U68765

Description

Salmonella typhimurium 5'-phosphoribosylglycinamide transformylase (purN) and 5'-phosphoribosyl-5-aminoimidazole synthetase (purI) genes, complete cds.

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
10744000_c3_102	1333	3253	309	930	1094	1.0e-110

Protein name
 probable Mn transport protein

Locus Name
 pir:G64063

Acc#
 G64063:C41833

Description

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
1181631_f1_2	1334	3254	558	1677	1333	4.9e-136

Protein name

Locus Name
 sp:60IM_PSEPU

Acc#
 P25754

Description

60 KD INNER-MEMBRANE PROTEIN

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
13703378_c3_117	1335	3255	95	288	163	4.7e-12

Protein name

Locus Name
 sp:YEAQ_ECOLI

Acc#
 P76246

Description

HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC REGION

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15031513_f3_43	1336	3256	479	1440	1390	4.5e-142

Protein name

Locus Name
 sp:THRC_METGL

Acc#
 P37145

Description

THREONINE SYNTHASE,

ORF Name	NTID	AAID	NT Length	AA Length	Score	Probability
15039077_c1_64	1337	3257	266	801	196	1.5e-15

Protein name

Locus Name
 gp:DNINTREG

Acc#
 X98546

Description

D.nodosus intB, regA, gepA, gepB, and gepC genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15665903_c1_59	1338	3258	281	846	1074	1.4e-108

Protein name

Locus Name

Acc#

sp:Y360_HAEIN

P44661

Description

HYPOTHETICAL PROTEIN HI0360

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15798825_c1_65	1339	3259	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19538327_c1_72	1340	3260	213	642	218	7.0e-18

Protein name

Locus Name

Acc#

sp:Y882_METJA

Q58292

Description

HYPOTHETICAL PROTEIN MJ0882

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
197188_f3_42	1341	3261	345	1038	659	1.3e-64

Protein name

Locus Name

Acc#

sp:FMT_PSEAE

O85732

Description

METHIONYL-TRNA FORMYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20197175_f3_44	1342	3262	415	1248	453	5.0e-47

Protein name

Locus Name

Acc#

sp:SMF_HAEIN

P43862

Description

SMF PROTEIN (DNA PROCESSING CHAIN A)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23440886_f2_27	1343	3263	602	1809	241	2.1e-19

Protein name

Locus Name

Acc#

sp:Y678_METJA

Q58091

Description

HYPOTHETICAL PROTEIN MJ0678

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
241290_f2_31	1344	3264	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24244010_c3_106	1345	3265	83	252	69	0.042

Protein name

Locus Name

Acc#

hypothetical protein Y105C5B.x

pir:T26400

T26400

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24253187_c3_107	1346	3266	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24255262_c2_96	1347	3267	430	1293	873	2.7e-87

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:C75339

C75339

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24256550_f3_40	1348	3268	165	498	465	4.7e-44

Protein name

Locus Name

Acc#

sp:YBAD_ECOLI

P25538

Description

HYPOTHETICAL 17.2 KD PROTEIN IN TSX-RIBG INTERGENIC REGION (ORF1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24337786_f3_48	1349	3269	311	936	657	2.1e-64

Protein name

Locus Name

Acc#

sp:ARGI_BRUAB

Q59174

Description

ARGINASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24417762_f1_18	1350	3270	62	189	74	0.030

Protein name

Locus Name

Acc#

sp:FM1A_SERMA

P22595

Description

TYPE-I FIMBRIAL PROTEIN SUBUNIT PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24489626_f2_21	1351	3271	474	1425	1058	6.8e-107

Protein name

Locus Name

Acc#

sp:THDF_PSEPU

P25755

Description

POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THDF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24643777_f2_22	1352	3272	352	1059	682	4.3e-78

Protein name

Locus Name

Acc#

sp:RIBD_ECOLI

P25539

Description

RIBOFLAVIN-SPECIFIC DEAMINASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24643937_f1_4	1353	3273	450	1353	695	2.0e-68

Protein name

Locus Name

Acc#

sp:SUN_HAEIN

P44788

Description

SUN PROTEIN (FMU PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
26603562_c2_86	1354	3274	303	912	1047	9.9e-106

Protein name

Locus Name

Acc#

sp:FECE_HAEIN

P44662

Description

IRON(III) DICITRATE TRANSPORT ATP-BINDING PROTEIN FECE HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2738783_f2_37	1355	3275	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2750262_f1_1	1356	3276	103	312	193	3.1e-15

Protein name

Locus Name

Acc#

hypothetical protein SCH24.04

pir:T36569

T36569

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29539015_c1_62	1357	3277	417	1254	666	2.3e-65

Protein name

Locus Name

Acc#

sp:YDHH_ECOLI

P77570

Description

HYPOTHETICAL 39.5 KD PROTEIN IN PDXH-SLYB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30739700_f1_7	1358	3278	211	636	244	1.2e-20

Protein name

Locus Name

Acc#

sp:YRDC_ECOLI

P45748

Description

HYPOTHETICAL 20.8 KD PROTEIN IN AROE-SMG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34088143_f3_55	1359	3279	106	321		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3913215_f2_26	1360	3280	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3939063_f2_23	1361	3281	225	678	519	8.8e-50

Protein name

Locus Name

Acc#

sp:RISA_PHOPO

P51961

Description

RIBOFLAVIN SYNTHASE ALPHA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3942213_c2_97	1362	3282	367	1104	930	2.5e-93

Protein name

Locus Name

Acc#

sp:GCH2_PHOLE

Q02008

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4785911_f2_29	1363	3283	435	1308	1321	9.1e-135

Protein name

Locus Name

Acc#

sp:OAT_DROAN

P49724

Description

ACID AMINOTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5214052_f3_53	1364	3284	411	1236	1096	6.4e-111

Protein name

Locus Name

Acc#

sp:SYN_HAEIN

P43836

Description

TYROSYL-TRNA SYNTHETASE, (TYROSINE--TRNA LIGASE) (TYRRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5282562_c1_63	1365	3285	265	798	693	3.2e-68

Protein name

Locus Name

Acc#

hypothetical protein jhp0330

pir:B71947

B71947

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6070166_f2_20	1366	3286	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6147028_c1_60	1367	3287	292	879	870	5.6e-87

Protein name

Locus Name

Acc#

sp:YFED_YERPE

Q56955

Description

CHELATED IRON TRANSPORT SYSTEM MEMBRANE PROTEIN YFED

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
839752_f1_19	1368	3288	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
867183_c1_68	1369	3289	128	387	107	2.7e-05

Protein name Locus Name Acc#

sp:YRAM_BACSU 007931

Description

HYPOTHETICAL 39.5 KD PROTEIN IN SIGZ-CSN INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1197077_f3_44	1370	3290	375	1128	178	8.2e-11

Protein name Locus Name Acc#

hypothetical protein TM0342 pir:D72388 D72388

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14641008_f3_46	1371	3291	271	816	360	6.2e-33

Protein name Locus Name Acc#

putative thiol:disulfide interchange protein gp:AF057031 AF057031

Description

Pseudomonas aeruginosa putative thiol:disulfide interchange protein precursor (dsbC) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15058126_f1_9	1372	3292	204	615	183	3.6e-14

Protein name Locus Name Acc#

hypothetical protein gp:AF088857 AF088857

Description

Vogesella indigofera indigoidine biosynthesis regulatory locus, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
158638_c3_82	1373	3293	89	270	350	7.2e-32

Protein name Locus Name Acc#
 sp:IMDH_ACICA P31002

Description

DEHYDROGENASE) (IMPDH) (IMPD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16992775_f2_22	1374	3294	61	186	85	0.00086

Protein name Locus Name Acc#
 gamma-carboxymuconolactone decarboxylase pir:B69129 B69129

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20353465_f2_21	1375	3295	167	504		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20734687_c2_78	1376	3296	297	894	642	8.2e-63

Protein name Locus Name Acc#
 sp:YAAJ_HAEIN P44555

Description

HYPOTHETICAL PROTEIN HI0183

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21672011_c1_54	1377	3297	61	186	55	0.0095

Protein name Locus Name Acc#
 sp:YY10_METJA Q60309

Description

HYPOTHETICAL PROTEIN MJECS10

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23439077_f1_5	1378	3298	177	534	103	0.0035

Protein name

ORF MSV035 hypothetical protein

Locus Name

gp:AF063866

Acc#

AF063866

Description

Melanoplus sanguinipes entomopoxvirus, complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
2347156_f1_8	1379	3299	1105	3318	1839	2.0e-286

Protein name

isoleucine--tRNA ligase,:isoleucyl-tRNA
synthetase

Locus Name

pir:SYECIT

Acc#

B64723:S40

549:A94277

:A91325:A9

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23652183_c1_56	1380	3300	777	2334	3955	0.0

Protein name

outer membrane protein CopB

Locus Name

gp:U69981

Acc#

U69981

Description

Moraxella catarrhalis strain O12E outer membrane protein CopB gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23865660_c2_77	1381	3301	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25506316_f1_14	1382	3302	228	687	554	1.7e-53

Protein name

Locus Name

Acc#

sp:YIHA_ECOLI

P24253:P76

771

Description

HYPOTHETICAL GTP-BINDING PROTEIN IN POLA-HEMN INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2584717_f3_43	1383	3303	87	264	127	3.1e-08

Protein name

gamma-carboxymuconolactone decarboxylase

Locus Name

pir:B69129

Acc#

B69129

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25942137_f2_29	1384	3304	185	558	296	3.8e-26

Protein name

Locus Name

sp:FKBX_PSEFL

Acc#

P21863

Description

(EC 5.2.1.8) (PPIASE) (ROTAMASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26364431_c1_49	1385	3305	117	354	300	1.4e-26

Protein name

Locus Name

pir:FEKRV

Acc#

S72167:S78
121:A00210

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32056506_c3_81	1386	3306	401	1206	1486	3.0e-152

Protein name

Locus Name

sp:IMDH_ACICA

Acc#

P31002

Description

DEHYDROGENASE) (IMPDH) (IMPD)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32477250_c1_65	1387	3307	443	1332	1422	1.8e-145

Protein name

Locus Name

sp:YCDG_ECOLI

Acc#

P75892

Description

HYPOTHETICAL 48.1 KD PROTEIN IN WRBA-PUTA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34665952_f2_28	1388	3308	177	534	371	4.3e-34

Protein name

Locus Name

Acc#

sp:LSPA_PSEFL

P17942

Description

PEPTIDASE) (SIGNAL PEPTIDASE II) (SPASE II)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4775762_f1_15	1389	3309	252	759	593	1.3e-57

Protein name

Locus Name

Acc#

sp:YRAL_ECOLI

P45528

Description

HYPOTHETICAL 31.3 KD PROTEIN IN AGAI-MTR INTERGENIC REGION (F286)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5910313_f2_30	1390	3310	392	1179	895	1.3e-89

Protein name

Locus Name

Acc#

homoserine O-acetyltransferase

gp:LMMETYX

Y10744

Description

L.meyer1 metY and metX genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5976592_f2_41	1391	3311	152	459	276	5.0e-24

Protein name

Locus Name

Acc#

LporfX

gp:LPU63641

U63641

Description

Legionella pneumophila rpoD operon LporfX, LpdnaG, and LprpoDgenes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
818765_f1_7	1392	3312	98	297		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9765832_f2_38	1393	3313	458	1377	1102	1.5e-111

Protein name

homoserine dehydrogenase

Locus Name

gp:L78665

Acc#

L78665

Description

Methylobacillus flagellatum aspartate aminotransferase (aat), membrane protein (orf-1), homoserine dehydrogenase (hom), and threonine synthase (thrC) thymidylate sythase (thyA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9773436_f2_31	1394	3314	215	648	117	0.00011

Protein name

probable 24-sterol C-methyltransferase,

Locus Name

pir:T03845

Acc#

T03845

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10423125_c2_44	1395	3315	124	375		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1069202_f2_13	1396	3316	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12933427_f2_5	1397	3317	131	396	239	4.1e-20

Protein name

Locus Name

Acc#

sp:DHSC_ECOLI

P10446

Description

SUCCINATE DEHYDROGENASE CYTOCHROME B-556 SUBUNIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20330461_f3_19	1398	3318	229	690	714	1.9e-70

Protein name Locus Name Acc#
fumarate reductase flavoprotein subunit gp:AB015757 AB015757

Description

Rhodoferrax fermentans genes for fumarate reductase subunits, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
214128_f2_9	1399	3319	763	2292	2566	1.1e-266

Protein name Locus Name Acc#
sp:ODO1_AZOV1 P20707

Description

KETOGLUTARATE DEHYDROGENASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21501557_f3_27	1400	3320	80	243		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21510931_f2_6	1401	3321	381	1146	1445	6.6e-148

Protein name Locus Name Acc#
fumarate reductase flavoprotein subunit gp:AB015757 AB015757

Description

Rhodoferrax fermentans genes for fumarate reductase subunits, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23469010_f3_25	1402	3322	62	189		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23855067_c3_53	1403	3323	183	552	76	0.018

Protein name putative adhesin MAA1 Locus Name gp:AF154922 Acc# AF154922

Description

Mycoplasma arthritidis strain 158 putative adhesin MAA1 (maal) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24241463_f2_10	1404	3324	68	207	131	2.6e-07

Protein name Locus Name sp:ODO1_HAEIN Acc# P45303

Description

KETOGLUTARATE DEHYDROGENASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24251441_f1_4	1405	3325	375	1128	129	5.8e-05

Protein name heme receptor Locus Name gp:VIBHUTA Acc# L27149

Description

Vibrio cholerae heme receptor (hutA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24427262_f2_8	1406	3326	123	372	234	2.6e-18

Protein name alpha-ketoglutarate dehydrogenase Locus Name gp:AF068740 Acc# AF068740

Description

Pseudomonas putida dihydrolipoamide succinyltransferase (kgdB) and alpha-ketoglutarate dehydrogenase (kgdA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26367192_f1_2	1407	3327	488	1467	1401	3.0e-143

Protein name dihydrolipoamide dehydrogenase Locus Name gp:PSELPDA Acc# M28356

Description

P.fluorescens dihydrolipoamide dehydrogenase (lpd) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26377042_f2_7	1408	3328	192	579	790	1.7e-78

Protein name

succinate dehydrogenase putative iron sulphur

Locus Name

gp:SPSDH

Acc#

Y13760

Description

Shewanella frigidimarina NCIMB400 sdhA, sdhB, sdhC, sdhD and sucAgenes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31439375_f1_1	1409	3329	135	408	275	6.3e-24

Protein name

Locus Name

sp:DHSD_ECOLI

Acc#

P10445

Description

SUCCINATE DEHYDROGENASE HYDROPHOBIC MEMBRANE ANCHOR PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4064425_f3_26	1410	3330	599	1800	123	8.1e-05

Protein name

Locus Name

sp:FOXA_SALTY

Acc#

Q56145

Description

FERRIOXAMINE B RECEPTOR PRECURSOR (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
584625_f2_11	1411	3331	420	1263	1194	2.6e-121

Protein name

dihydrolipoamide
S-succinyltransferase, :2-oxoglutarate
dehydrogenase complex chain E2:succinyl

Locus Name

p1r:S07779

Acc#

S07779:S63
511

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9928130_c1_34	1412	3332	141	426	116	8.6e-07

Protein name

microfilarial sheath protein SHP3 precursor

Locus Name

gp:AF030944

Acc#

AF030944:U

Description

43510

Brugia malayi microfilarial sheath protein SHP3a (Bmshp3a) and microfilarial sheath protein SHP3 precursor (Bmshp3) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12619081_c3_114	1413	3333	147	444	205	1.7e-16

Protein name

Locus Name

sp:YBAN_ECOLI

Acc#

P45808:P77

Description

478

HYPOTHETICAL 14.8 KD PROTEIN IN PRIC-APT INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12897562_c1_73	1414	3334	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1359776_c2_91	1415	3335	67	204		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14064028_c2_105	1416	3336	269	810	182	4.5e-14

Protein name

Locus Name

sp:YEAB_ECOLI

Acc#

P43337

Description

HYPOTHETICAL 21.4 KD PROTEIN IN PABB-SDAA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14657782_c2_104	1417	3337	173	522	333	4.5e-30

Protein name

Locus Name

Acc#

sp:BID2_HAEIN

P45248

Description

2) (DTB SYNTHETASE 2) (DTBS 2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14719437_f1_22	1418	3338	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14882713_c3_116	1419	3339	287	864	289	8.1e-30

Protein name

Locus Name

Acc#

sp:BIOC_HAEIN

P45249

Description

POTATIVE BIOTIN SYNTHESIS PROTEIN BIOC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16464750_c2_86	1420	3340	326	981	123	6.0e-05

Protein name

Locus Name

Acc#

sp:ZIPA_ECOLI

P77173

Description

CELL DIVISION PROTEIN ZIPA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16532256_f1_1	1421	3341	80	243	95	0.0015

Protein name

Locus Name

Acc#

ubiquitin protein ligase

pir:T39585

T39585

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19572130_f3_58	1422	3342	310	933	1010	8.2e-102

Protein name

Locus Name

Acc#

sp:CYSM_ECOLI

P16703

Description

(O-ACETYLSELINE (THIOL)-LYASE B) (CSASE B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19734630_f2_40	1423	3343	533	1602	400	3.1e-57

Protein name

Locus Name

Acc#

sp:YGCA_HAEIN

P44643

Description

HYPOTHETICAL RNA METHYLTRANSFERASE HI0333,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20507762_f1_13	1424	3344	290	873	548	7.5e-53

Protein name

Locus Name

Acc#

sp:DPSD_ECOLI

P10740

Description

PHOSPHATIDYLSERINE DECARBOXYLASE PROENZYME,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20839062_c2_92	1425	3345	444	1335	482	1.3e-48

Protein name

Locus Name

Acc#

sp:DEAD_HAEIN

P44586

Description

ATP-DEPENDENT RNA HELICASE DEAD HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22144026_f1_26	1426	3346	284	855	443	4.3e-41

Protein name

Locus Name

Acc#

sp:RELA_HAEIN

P44644

Description

(PPGPP SYNTHETASE I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22147806_f3_47	1427	3347	421	1266	866	1.5e-86

Protein name

Locus Name

Acc#

sp:YGIC_ECOLI

P24196

Description

(O386)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22691300_c2_99	1428	3348	612	1839	688	7.1e-72

Protein name

Locus Name

Acc#

sensor kinase rtpA

gp:AB002529

AB002529

Description

Pseudomonas tolaasii gene for sensor kinase rtpA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22890917_f2_33	1429	3349	258	777	196	1.5e-15

Protein name

Locus Name

Acc#

sp:YBEN_ECOLI

P52085

Description

HYPOTHETICAL 24.5 KD PROTEIN IN PHPB-HOLA INTERGENIC REGION (ORFUU)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23478458_c2_103	1430	3350	441	1326	1328	1.7e-135

Protein name

Locus Name

Acc#

BioA

gp:AF191556

AF191556

Description

Xenorhabdus nematophilus YbhE (ybhE) gene, partial cds; Var1 (var1) and BioA (bioA) genes, complete cds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24097812_c1_83	1431	3351	208	627	462	9.7e-44

Protein name

Locus Name

Acc#

sp:SSB_HAEIN

P44409

Description

SINGLE-STRAND BINDING PROTEIN (SSB) (HELIX-DESTABILIZING PROTEIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24225088_f2_39	1432	3352	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25587827_c1_79	1433	3353	400	1203	888	7.0e-89

Protein name

Locus Name

Acc#

sp:BI0F_HAEIN

P44422

Description

LIGASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26192160_f3_64	1434	3354	532	1599	894	1.6e-89

Protein name

Locus Name

Acc#

sp:RELA_ECOLI

P11585

Description

(PPGPP SYNTHETASE I)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29298385_f1_8	1435	3355	211	636	380	4.7e-35

Protein name

Locus Name

Acc#

gp:U90439

U90439:AE0
02093

Description

Arabidopsis thaliana chromosome II section 227 of 255 of the complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33708181_c1_75	1436	3356	411	1236	391	3.2e-36

Protein name

Locus Name

Acc#

putative histidine kinase

gp:PST249741

AJ249741

Description

Pseudomonas stutzeri JM300 gacS (partial) and ggtB (partial) genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33728258_c3_117	1437	3357	78	237	85	0.0019

Protein name

Locus Name

Acc#

sp:BD2_HAEIN

P45248

Description

2) (DTB SYNTHETASE 2) (DTBS 2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35173953_f1_7	1438	3358	152	459	237	6.8e-20

Protein name

Locus Name

Acc#

sp:YBEB_ECOLI

P05848:P77
107

Description

HYPOTHETICAL 11.6 KD PROTEIN IN MRDA-PHPB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35183451_f2_38	1439	3359	261	786	259	3.1e-22

Protein name

Locus Name

Acc#

hypothetical protein jhp0628

pir:B71907

B71907

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4147637_c3_120	1440	3360	990	2973	3281	0.0

Protein name

Locus Name

Acc#

sp:UVRA_ECOLI

P07671:P76
788

Description

EXCINUCLEASE ABC SUBUNIT A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4199006_f3_56	1441	3361	69	210	52	0.022

Protein name

Locus Name

Acc#

NADH dehydrogenase subunit 4

sp:AF026170

AF026170

Description

Teius teyou NADH dehydrogenase subunit 4 (ND4) gene, partial cds;and tRNA-His, tRNA-Ser, and tRNA-Leu genes, complete sequence,mitochondrial genes for mitochondrial products.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4328431_f3_65	1442	3362	305	918	542	3.2e-52

Protein name

Locus Name

Acc#

sp:FPG_NEIME

P55044

Description

GLYCOSYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4867812_c3_118	1443	3363	154	465	318	1.8e-28

Protein name

Locus Name

Acc#

sp:YIHZ_ECOLI

P32147

Description

HYPOTHETICAL 15.9 KD PROTEIN IN RBN-FDHE INTERGENIC REGION (O145)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
892177_c1_70	1444	3364	169	510	331	7.4e-30

Protein name

Locus Name

Acc#

gp:D83386

D83386

Description

Shewanella violacea rhIE, cydD, cydC and putA genes, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16847336_f3_5	1445	3365	177	534	633	7.3e-62

Protein name

Locus Name

Acc#

DNA-directed RNA polymerase alpha chain

gp:AF047025

AF047025

Description

Pseudomonas aeruginosa ribosomal protein S4 (rpsD) gene, partial cds; DNA-directed RNA polymerase alpha chain (rpoA), ribosomal large subunit protein L17 (rplQ), and catalase isozyme A (katA) genes, complete cds; and bacterioferritin (bfr) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16976442_c3_13	1446	3366	239	720	359	8.0e-33

Protein name

Locus Name

Acc#

sp:YFCM_ECOLI

Description

P76938:P76
497

HYPOTHETICAL 21.1 KD PROTEIN IN FABB-MEPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24226655_f2_3	1447	3367	165	498	499	1.2e-47

Protein name

Locus Name

Acc#

DNA-directed RNA polymerase alpha chain

gp:AF047025

AF047025

Description

Pseudomonas aeruginosa ribosomal protein S4 (rpsD) gene, partial cds; DNA-directed RNA polymerase alpha chain (rpoA), ribosomal large subunit protein L17 (rplQ), and catalase isozyme A (kata) genes, complete cds; and bacterioferritin (bfr) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24317501_f2_4	1448	3368	83	252	354	2.7e-32

Protein name

Locus Name

Acc#

sp:RL17_PSEAE

052761

Description

50S RIBOSOMAL PROTEIN L17

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3001693_f2_2	1449	3369	217	654	683	3.7e-67

Protein name

Locus Name

Acc#

ribosomal protein S4

pir:A64095

A64095

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4867143_c1_9	1450	3370	191	576	314	4.7e-28

Protein name

Locus Name

Acc#

probable translation factor yci0

pir:F64874

F64874

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6033377_c3_14	1451	3371	94	285	84	0.035

Protein name

hypothetical protein C34F6.9

Locus Name

pir:T19736

Acc#

T19736

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10437517_c1_70	1452	3372	62	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11808576_c2_83	1453	3373	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1359677_f2_17	1454	3374	373	1122	969	1.8e-97

Protein name

uroporphyrinogen decarboxylase

Locus Name

qp:ECOUW89

Acc#

U00006

Description

E. coli chromosomal region from 89.2 to 92.8 minutes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14898317_c3_94	1455	3375	591	1776	1769	3.1e-182

Protein name

Locus Name

Acc#

sp:SYD ECOLI

P21889

Description

(ASPRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16522206_c1_56	1456	3376	207	624		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16614042_c3_107	1457	3377	125	378	142	7.9e-10

Protein name Locus Name Acc#

hypothetical protein sir1903 pir:S77514 S77514

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
175817_f3_32	1458	3378	442	1329	1020	7.2e-103

Protein name Locus Name Acc#

glyceraldehyde-3-phosphate dehydrogenase gp:AF058302 AF058302

Description

Streptomyces roseofulvus frenolicin biosynthetic gene cluster, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20984532_c1_68	1459	3379	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2142151_f3_38	1460	3380	252	759	421	2.1e-39

Protein name Locus Name Acc#

anion transport ABC transporter (ATP-bind1) homolog ytlC pir:C69995 C69995

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23437558_f2_24	1461	3381	348	1047	946	5.0e-95

Protein name

3-phosphoserine aminotransferase

Locus Name

gp:AF038578

Acc#

AF038578:M

Description

73971:M355

45

Pseudomonas stutzeri gyrase A subunit (gyrA) gene, partial cds;3-phosphoserine aminotransferase (serC), chorismatase/prephenate dehydratase (aroQp/pheA), imidazole acetol phosphate aminotransferase (hisHb), and cyclohexadienyl dehydrogenase (tyrAc) genes, complete cds; and 5-enolpyruvylshikimate 3-P synthase (aroF) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23526888_f1_7	1462	3382	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23642875_f3_39	1463	3383	255	768		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24103137_f2_16	1464	3384	409	1230	1079	4.0e-109

Protein name

Locus Name

Acc#

sp:YHBZ_HAEIN

P44915

Description

HYPOTHETICAL 43.4 KD GTP-BINDING PROTEIN HI0877

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24272135_c3_103	1465	3385	174	525	295	4.8e-26

Protein name Lrp-family transcriptional regulators Locus Name gp:D89015 Acc# D89015

Description

Pseudomonas putida genes for MdeR, MdeA and MdeB, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24410038_f2_19	1466	3386	443	1332	743	1.6e-73

Protein name proteinase DO Locus Name pir:H71936 Acc# H71936

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25662512_c3_98	1467	3387	304	915	532	3.7e-51

Protein name Locus Name sp:YJJP_ECOLI Acc# P39402

Description

HYPOTHETICAL 30.5 KD PROTEIN IN DNAT-BGLJ INTERGENIC REGION (F277)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25665963_f1_5	1468	3388	264	795	444	7.8e-42

Protein name Locus Name sp:GL02_ECOLI Acc# Q47677

Description

II) (GLX II)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2757750_f3_47	1469	3389	72	219	73	0.016

Protein name Locus Name gp:AB021078 Acc# AB021078

Description

plasmid ColIb-P9 DNA, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31412958_f2_23	1470	3390	250	753		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33394002_f2_30	1471	3391	507	1524	79	0.036

Protein name

Locus Name

Acc#

cytochrome-c oxidase, chain I RP405

pir:D71698

D71698

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35181680_c3_95	1472	3392	356	1071	267	4.5e-23

Protein name

Locus Name

Acc#

gp:PFY14568

Y14568

Description

Pseudomonas fluorescens tag gene and partial glyQ, htrB genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4009750_c1_69	1473	3393	221	666	279	2.4e-24

Protein name

Locus Name

Acc#

hypothetical protein

pir:S76551

S76551

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4165952_f3_34	1474	3394	82	249		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5115943_f2_21	1480	3400	330	993	585	9.0e-57

Protein name

hypothetical protein TM0484

Locus Name

pir:C72369

Acc#

C72369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5266588_f2_29	1481	3401	878	2637	2754	1.3e-286

Protein name

UspA1

Locus Name

gp:AF113606

Acc#

AF113606

Description

Moraxella catarrhalis strain ATCC25238 UspA1 (uspA1) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
802137_f3_37	1482	3402	261	786	459	2.0e-43

Protein name

ABC transporter, permease protein, cystW family

Locus Name

pir:D72369

Acc#

D72369

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
894387_c2_80	1483	3403	160	483	313	6.0e-28

Protein name

Locus Name

sp:YJJP_HAEIN

Acc#

P44520

Description

HYPOTHETICAL PROTEIN HI0108

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
976558_f2_18	1484	3404	61	186		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10740682_c2_12	1485	3405	297	894	678	1.3e-66

Protein name

probable acyl-CoA dehydrogenase

Locus Name

pir:B75282

Acc#

B75282

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16829202_f3_8	1486	3406	251	753	185	2.2e-14

Protein name

Locus Name

sp:PABC_ECOLI

Acc#

P28305

Description

4-AMINO-4-DEOXYCHORISMATE LYASE, (ADC LYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25421887_f1_2	1487	3407	188	567		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34160918_f3_7	1488	3408	64	195		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6365631_c3_13	1489	3409	275	828	475	4.1e-45

Protein name

shikimate dehydrogenase

Locus Name

gp:NPU82846

Acc#

U82846

Description

Neisseria pharyngis var. flava shikimate dehydrogenase (aroE) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12156514_c1_16	1490	3410	162	489	336	2.2e-30

Protein name

Locus Name

Acc#

sp:RSTA_ECOLI

P52108

Description

TRANSCRIPTIONAL REGULATORY PROTEIN RSTA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15625078_c1_19	1491	3411	179	537	444	7.8e-42

Protein name

Locus Name

Acc#

sp:TRMD_SERMA

P36244

Description

METHYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23468928_c1_18	1492	3412	191	576	295	4.8e-26

Protein name

Locus Name

Acc#

sp:RIMM_HAEIN

P44568

Description

16S RRNA PROCESSING PROTEIN RIMM

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23859377_f1_4	1493	3413	502	1509	525	2.0e-50

Protein name

Locus Name

Acc#

EnvZ protein

gp:YEOMPR

Y08950

Description

Y.enterocolitica ompR and envZ genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3961587_c2_21	1494	3414	86	261	279	2.4e-24

Protein name

Locus Name

Acc#

sp:RS16_HAEIN

P44382

Description

30S RIBOSOMAL PROTEIN S16

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
964692_c3_22	1495	3415	598	1797	442	1.3e-41

Protein name

Locus Name

Acc#

sp:RSTB_ECOLI

P18392

Description

SENSOR PROTEIN RSTB,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10676257_f2_68	1496	3416	393	1182	1212	3.2e-123

Protein name

Locus Name

Acc#

sp:PUR9_HAEIN

P43852

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10736257_f3_80	1497	3417	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12556337_f1_31	1498	3418	128	387	477	2.5e-45

Protein name

Locus Name

Acc#

sp:PUR9_ECOLI

P15639

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1272283_f2_60	1499	3419	183	552	244	7.9e-20

Protein name

Locus Name

Acc#

sp:AARF_ECOLI

P27854:P27
855:P76764
:P27853

Description

UBIQUINONE BIOSYNTHESIS PROTEIN AARF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
131700_c1_108	1500	3420	255	768	215	1.4e-16

Protein name

putative peptidyl-prolyl cis-trans isomerase

Locus Name

gp:ASAJ2316

Acc#

AJ002316

Description

Acinetobacter sp. ADP1 alkR & alkM genes, ORF1 & ORF4.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13876562_c1_128	1501	3421	75	228	73	0.016

Protein name

immunoglobulin kappa light chain variable

Locus Name

gp:AF131156

Acc#

AF131156

Description

Mus musculus immunoglobulin kappa light chain variable region gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13947127_c3_217	1502	3422	584	1755	1216	1.6e-163

Protein name

Locus Name

sp:SYQ_HAEIN

Acc#

P43831

Description

(GLNRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14852035_c1_129	1503	3423	85	258	70	0.033

Protein name

tat protein

Locus Name

gp:HIVU86775

Acc#

U86775

Description

HIV-1 clone ZAM184-5.2 from Zambia, tat protein (tat) gene, partial cds, rev protein (rev), vpu protein (vpu), and envelope glycoprotein (env) genes, complete cds and nef protein (nef) pseudogene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15663417_f2_42	1504	3424	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16583425_c1_131	1505	3425	326	981	535	1.8e-51

Protein name

yfjB protein

Locus Name

pir:B65040

Acc#

B65040

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19632665_c2_160	1506	3426	696	2091	633	2.3e-79

Protein name

Locus Name

sp:COPA_ENTHR

Acc#

P32113:Q47
841

Description

COPPER/POTASSIUM-TRANSPORTING ATPASE A,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19706557_c3_193	1507	3427	216	651	148	4.8e-08

Protein name

probable component of cation transport for
cbb3-type oxidase

Locus Name

pir:E71813

Acc#

E71813

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21753552_c3_220	1508	3428	168	507		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2197962_f1_11	1509	3429	122	369		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22145253_c2_177	1510	3430	210	633	592	1.6e-57

Protein name

Locus Name

Acc#

sp:ORN_HAEIN

P45340

Description

OLIGORIBONUCLEASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22272900_f1_5	1511	3431	227	684	263	1.2e-22

Protein name

Locus Name

Acc#

hypothetical protein

gp:PST243354

AJ243354

Description

Pseudomonas stutzeri hyp1 and comA genes and putative tolQ, exbB, tolR and exbD genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22285902_c3_212	1512	3432	229	690	299	1.8e-26

Protein name

Locus Name

Acc#

transposase slr2062:protein slr2062:protein
slr2062

pir:S74909

S74909

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22710402_c2_154	1513	3433	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23457632_f3_90	1514	3434	295	888	885	1.5e-88

Protein name

Locus Name

Acc#

sp:UBIE_ECOLI

P27851

Description

(EC 2.1.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23475002_f1_9	1515	3435	182	549	121	4.8e-06

Protein name

Locus Name

Acc#

sp:CUTF_ECOLI

P40710

Description

COPPER HOMEOSTASIS PROTEIN CUTF PRECURSOR (LIPOPROTEIN NLPE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23554676_f1_16	1516	3436	384	1155	692	4.1e-68

Protein name

Locus Name

Acc#

sp:AARF_ECOLI

P27854:P27

855:P76764

:P27853

Description

UBIQUINONE BIOSYNTHESIS PROTEIN AARF

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23634656_c3_200	1517	3437	97	294	147	2.3e-10

Protein name

Locus Name

Acc#

sp:YEAC_ECOLI

P76231

Description

HYPOTHETICAL 10.3 KD PROTEIN IN ANSA-GAPA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24015950_c1_147	1518	3438	201	606	207	1.0e-16

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF157493

AF157493

Description

Zymomonas mobilis ZM4 fosmid clone 42D7, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24259702_f1_10	1519	3439	500	1503	275	2.4e-23

Protein name

Locus Name

Acc#

sp:YF46_ARCFU

O28726

Description

HYPOTHETICAL PROTEIN AF1546

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24303583_f1_30	1520	3440	93	282	169	1.1e-12

Protein name

small DNA binding protein Fis

Locus Name

gp:AF040379

Acc#

AF040379

Description

Proteus vulgaris ribosomal protein L11 methyltransferase (prmA) gene, partial cds; yhdG homolog gene, complete cds; and small DNA binding protein Fis (fis) gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24306510_c3_209	1521	3441	224	675	443	1.0e-41

Protein name

Locus Name

sp:EST2_PSEFL

Acc#

Q53547

Description

CARBOXYLESTERASE 2, (ESTERASE II)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24613752_c2_168	1522	3442	241	726	813	6.2e-81

Protein name

superoxide dismutase, (Mn):SodA protein

Locus Name

pir:JC6542

Acc#

JC6542

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24614125_f2_65	1523	3443	816	2451	1566	1.0e-160

Protein name

penicillin-binding protein 1B

Locus Name

gp:AF147449

Acc#

AF147449

Description

Pseudomonas aeruginosa strain PA01 penicillin-binding protein 1B(ponB) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24640762_f3_79	1524	3444	388	1167	1412	2.1e-144

Protein name

Locus Name

sp:METK_ECOLI

Acc#

P04384:P30

869

Description

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25551385_f1_17	1525	3445	175	528	298	2.3e-26

Protein name

adenine phosphoribosyltransferase,:protein
sll1430:protein sll1430

Locus Name

pir:S75440

Acc#

S75440

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25665962_f1_8	1526	3446	115	348	75	0.0099

Protein name

glutamyl-tRNA (Gln) amidotransferase subunit
C

Locus Name

pir:D70484

Acc#

D70484

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29687660_f3_88	1527	3447	310	933	441	1.6e-41

Protein name

hypothetical protein

Locus Name

pir:S76006

Acc#

S76006

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30650250_f1_12	1528	3448	298	897	664	3.8e-65

Protein name

conserved hypothetical protein

Locus Name

pir:A75256

Acc#

A75256

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31541442_c3_183	1529	3449	317	954	338	6.5e-30

Protein name

putative peptidyl-prolyl cis-trans isomerase

Locus Name

gp:ASAJ2316

Acc#

AJ002316

Description

Acinetobacter sp. ADP1 alkR & alkM genes, ORF1 & ORF4.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32694687_c2_181	1530	3450	140	423	117	2.0e-06

Protein name

Locus Name

Acc#

sp:YPBB_BACSU

P50728

Description

HYPOTHETICAL 40.7 KD PROTEIN IN FER-RECQ INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33213555_c3_216	1531	3451	60	183	106	1.3e-05

Protein name

Locus Name

Acc#

gp:ECU82664

U82664

Description

Escherichia coli minutes 9 to 11 genomic sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33245927_c3_213	1532	3452	229	690	606	5.3e-59

Protein name

Locus Name

Acc#

sp:YCFV_ECOLI

P75957

Description

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YCFV

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33394050_f3_76	1533	3453	269	810	340	8.2e-31

Protein name

Locus Name

Acc#

sp:YBBF_ECOLI

P43341:P77
440

Description

HYPOTHETICAL 26.9 KD PROTEIN IN PURE-PP1B INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3465_f3_89	1534	3454	71	216		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3906561_f1_18	1535	3455	248	747	311	9.7e-28

Protein name

Locus Name

Acc#

gp:STMBLDA

M80628

Description

Streptomyces griseus transfer RNA-Leu (bldA) gene and ORF, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3910693_f2_39	1536	3456	172	519	526	1.6e-50

Protein name

Locus Name

Acc#

sp:CYPB_ECOLI

P23869:P78
052

Description

(ROTAMASE B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3944178_f2_52	1537	3457	328	987		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3953218_c1_125	1538	3458	943	2832	156	1.1e-10

Protein name

Locus Name

Acc#

PhoC protein

gp:KPN250377

AJ250377

Description

Klebsiella pneumoniae partial selD gene for SelD protein and phoCgene for PhoC protein.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3991527_f2_67	1539	3459	2142	6429	577	4.0e-51

Protein name

Locus Name

Acc#

gp:U41852

U41852

Description

Haemophilus influenzae hsf gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4322793_f2_57	1540	3460	217	654		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4410943_c3_219	1541	3461	91	276	103	1.1e-05

Protein name

Locus Name

Acc#

sp:YGFY_ECOLI

Q46825

Description

HYPOTHETICAL 10.5 KD PROTEIN IN FLDB-BGLA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4688887_c3_211	1542	3462	452	1359	142	7.9e-07

Protein name

Locus Name

Acc#

metal transporter Nramp4

gp:AF202540

AF202540

Description

Arabidopsis thaliana metal transporter Nramp4 mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4782812_c1_141	1543	3463	147	444	95	0.011

Protein name

Locus Name

Acc#

hypothetical protein TM1026

pir:A72303

A72303

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4798430_c1_151	1544	3464	453	1362	447	7.2e-62

Protein name

Locus Name

Acc#

gp:SC9745

Z38114:Z71
257

Description

S.cerevisiae chromosome XIII cosmid 9745.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5125318_c3_206	1545	3465	356	1071	184	5.0e-21

Protein name

Locus Name

Acc#

gp:ATAC007168

AC007168

Description

Arabidopsis thaliana chromosome II BAC T26C19 genomic sequence, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5192757_c1_144	1546	3466	425	1278	734	1.5e-72

Protein name

Locus Name

Acc#

sp:YCFW_ECOLI

P75958

Description

HYPOTHETICAL 45.3 KD PROTEIN IN MFD-COBB INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5343752_f3_101	1547	3467	316	951	630	1.5e-61

Protein name

Locus Name

Acc#

sp:PRMA_ECOLI

P28637:P76

680:P76681

Description

RIBOSOMAL PROTEIN L11 METHYLTRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7042580_c1_142	1548	3468	75	228		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7312717_f3_77	1549	3469	75	228	77	0.028

Protein name

Locus Name

Acc#

conserved hypothetical protein 262

pir:S59078

S59078

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
822680_c3_218	1550	3470	417	1254	675	8.8e-82

Protein name

glyceraldehyde-3-phosphate dehydrogenase

Locus Name

gp:BACPGKTIMG

Acc#

M87647

Description

Bacillus megaterium glyceraldehyde-3-phosphate dehydrogenase (gap), phosphoglycerate kinase (pgk), and triose phosphate isomerase (tpi) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9767325_f3_82	1551	3471	147	444	476	3.2e-45

Protein name

transposase homolog A

Locus Name

gp:HPU95957

Acc#

U95957

Description

Helicobacter pylori insertion sequence IS606 transposase homologs A (tnpA) and B (tnpB) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12635413_f3_5	1552	3472	813	2442	1030	4.2e-129

Protein name

Locus Name

sp:UP05_ECOLI

Acc#

P39170:P39
181:P77465

Description

UNKNOWN PROTEIN FROM 2D-PAGE SPOTS M62/M63/O3/O9/T35 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31671880_f1_2	1553	3473	185	558	360	6.2e-33

Protein name

FabZ

Locus Name

gp:NMU79481

Acc#

U79481

Description

Neisseria meningitidis UDP-3-O- (R-3-hydroxymyristoyl)-glucosamineN-acyltransferase (lpxD) gene, partial cds, and 3(R)-hydroxymyristoyl acyl carrier protein dehydrase (fabZ) and UDP-N-acetylglucosamine acyltransferase (lpxA) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36148427_f3_8	1554	3474	67	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4412963_f2_4	1555	3475	185	558	470	1.4e-44

Protein name

Locus Name

Acc#

sp:LPXA_ECOLI

P10440:P78
243

Description

(EC 2.3.1.129) (UDP-N-ACETYLGLUCOSAMINE ACYLTRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4687640_f2_3	1556	3476	340	1023	667	1.8e-65

Protein name

Locus Name

Acc#

sp:LPXD_HAEIN

P43888

Description

(EC 2.3.1.-)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11978127_f1_2	1557	3477	379	1140	811	1.0e-80

Protein name

Locus Name

Acc#

sp:YECF_ECOLI

P76291:007
983

Description

HYPOTHETICAL 37.0 KD PROTEIN IN ASPS-BISZ INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14658562_f3_6	1558	3478	309	930	835	2.9e-83

Protein name

Locus Name

Acc#

sp:YEDI_ECOLI

P46125:P76
332

Description

HYPOTHETICAL 32.2 KD PROTEIN IN DSRB-VSR INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23714375_f3_8	1559	3479	100	303	70	0.033

Protein name

outer membrane protein H.8 precursor

Locus Name

pir:S04157

Acc#

S04157

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24253427_f3_7	1560	3480	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24322153_f3_5	1561	3481	257	774	475	4.1e-45

Protein name

Locus Name

Acc#

sp:YECO_HAEIN

P43985:P43
986

Description

HYPOTHETICAL PROTEIN HI0319/320

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24804651_c2_16	1562	3482	62	189	171	3.1e-12

Protein name

Locus Name

Acc#

sp:SSP2_PLAYO

Q01443

Description

SPOROZOITE SURFACE PROTEIN 2 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35181956_c1_11	1563	3483	251	756		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3955437_c2_19	1564	3484	73	219	138	2.1e-09

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
peptide methionine sulfoxide reductase	pir:E75345	E75345

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5117337_f3_9	1565	3485	379	1140	1148	2.0e-116

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
serine-pyruvate aminotransferase	pir:F75269	F75269

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1063441_c3_193	1566	3486	442	1329	272	1.4e-21

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
hypothetical protein 25	pir:T13514	T13514

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10650681_c3_218	1567	3487	102	309	72	1.0e-05

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>
unknown	gp:AF050676	AF050676

Description

Pseudomonas aeruginosa lipoprotein (oprX) and ferric uptake regulator (fur) genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
119027_c2_166	1568	3488	95	288		

<u>Protein name</u>	<u>Locus Name</u>	<u>Acc#</u>

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1227302_c3_221	1569	3489	90	273	85	0.012

Protein name

probable fatty-acid--CoA ligase, fadD7

Locus Name

pir:C69471

Acc#

C69471

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12773910_c2_171	1570	3490	116	351		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12973332_f1_18	1571	3491	63	192		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12992125_c2_170	1572	3492	152	459		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13085160_c3_196	1573	3493	236	711		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1371003_f3_87	1574	3494	413	1242	1088	4.5e-110

Protein name

Na+/H+-exchanging protein:Na+/H+ antiporter

Locus Name

pir:JX0360

Acc#

JX0360

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14647033_c3_209	1575	3495	192	579	128	1.8e-07

Protein name

muramoyl-pentapeptide carboxypeptidase

Locus Name

pir:T34747

Acc#

T34747

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14745253_c3_214	1576	3496	468	1407	596	6.1e-58

Protein name

hypothetical protein Rv3734c

Locus Name

pir:G70797

Acc#

G70797

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15633253_c1_149	1577	3497	150	453		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16485906_c3_192	1578	3498	484	1455	207	2.3e-14

Protein name

Locus Name

Acc#

sp:VG17_BPMD2

O64210

Description

MAJOR HEAD PROTEIN GPI7

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16595716_f2_69	1579	3499	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16597827_c1_133	1580	3500	205	618	92	0.022

Protein name putative prohead protease Locus Name gp:AF181080 Acc# AF181080

Description

Rhodobacter capsulatus putative large terminase, putative portalprotein, and putative prohead protease genes, complete cds; andputative capsid protein gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19547875_c1_157	1581	3501	124	375	189	8.2e-15

Protein name mono-heme c-type cytochrome ScyA Locus Name gp:AF044582 Acc# AF044582

Description

Shewanella putrefaciens NrfG homolog gene, partial cds; andmono-heme c-type cytochrome ScyA (scyA), cytochrome c maturationprotein A (ccmA), cytochrome c maturation protein B (ccmB),cytochrome c maturation protein C (ccmC), cytochrome c maturationprotein D (ccmD), and cytochrome c maturation protein E (ccmE)genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19697265_c2_179	1582	3502	65	198	75	0.020

Protein name Locus Name sp:YC67_ASTLO Acc# P34778

Description

HYPOTHETICAL 20.1 KD PROTEIN YCF67 (ORF170)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20917082_f3_105	1583	3503	71	216		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21663410_f1_17	1584	3504	170	513		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22351557_c3_191	1585	3505	89	270	70	0.0039

Protein name

Locus Name

Acc#

hypothetical protein F26B6.23

pir:T01147

T01147

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22381542_c3_199	1586	3506	257	774	457	3.3e-43

Protein name

Locus Name

Acc#

minor tail protein L homolog:protein gp18

pir:T13104

T13104

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23437561_f2_52	1587	3507	690	2073	1985	4.0e-205

Protein name

Locus Name

Acc#

sp:SYM_HAEIN

P43828

Description

(METRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23549217_c1_144	1588	3508	192	579	113	5.4e-05

Protein name

Locus Name

Acc#

hypothetical protein

pir:T14651

T14651

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23847257_c2_167	1589	3509	125	378		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24316886_f3_115	1590	3510	151	456	356	1.7e-32

Protein name

Locus Name

Acc#

sp:YDCQ_ECOLI

P76107

Description

HYPOTHETICAL 16.1 KD PROTEIN IN TEHB-ANSP INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24415876_f2_48	1591	3511	154	465		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24417540_c2_187	1592	3512	209	630	600	2.3e-58

Protein name

Locus Name

Acc#

gp:XCRPFB

Y09700

Description

X.campestris rpfB gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24431265_c2_182	1593	3513	486	1461	1261	2.1e-128

Protein name

Locus Name

Acc#

sp:SYC_ECOLI

P21888

Description

(CYSRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24614431_c2_173	1594	3514	169	510		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24631552_c2_181	1595	3515	271	816	723	2.1e-71

Protein name Locus Name Acc#

thiamin biosynthesis protein thiG pir:B70487 B70487

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24882676_c2_163	1596	3516	198	597	261	1.9e-22

Protein name Locus Name Acc#

sp:YE18_HAEIN P44189

Description

HYPOTHETICAL PROTEIN HI1418

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25397700_c1_148	1597	3517	221	666	388	6.7e-36

Protein name Locus Name Acc#

minor tail protein gp20 pir:T13106 T13106

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25493762_c1_161	1598	3518	60	183		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25584627_c3_216	1599	3519	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2581542_c3_213	1600	3520	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26819002_c1_141	1601	3521	90	273	72	0.020

Protein name

Locus Name

Acc#

hypothetical protein yorB

pir:T12887

T12887:C69
922

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
276927_f2_58	1602	3522	330	993	111	0.0016

Protein name

Locus Name

Acc#

sp:FINQ_ECOLI

P18809

Description

FINQ PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2792176_c2_180	1603	3523	112	339	112	1.2e-06

Protein name

Locus Name

Acc#

sp:YRK_FACSU

P54433

Description

HYPOTHETICAL 20.7 KD PROTEIN IN BLTR-SPOIIC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29337908_f1_37	1604	3524	82	249		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
31678827_c3_222	1605	3525	244	735	527	1.3e-50

Protein name Locus Name Acc#

long-chain-fatty-acid-CoA ligase gp:AF150669 AF150669

Description

Pseudomonas putida long-chain-fatty-acid-CoA ligase (fadD) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
32062552_f3_102	1606	3526	61	186	54	0.0065

Protein name Locus Name Acc#

sp:Y683_METJA Q58096

Description

HYPOTHETICAL PROTEIN MJ0683

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3207751_f3_103	1607	3527	126	381		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
35187543_c3_217	1608	3528	378	1137	105	0.0058

Protein name Locus Name Acc#

AdcB protein gp:SPADCA Z71552

Description

Streptococcus pneumoniae adcRCBA operon.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3937813_c1_158	1609	3529	233	702	368	8.9e-34

Protein name

Locus Name

Acc#

sp:CYC4_PSEST

Q52369

Description

CYTOCHROME C4 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
402217_c3_194	1610	3530	161	486		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4069212_c3_195	1611	3531	118	357	83	0.017

Protein name

Locus Name

Acc#

sp:Y182_METJA

Q57641

Description

HYPOTHETICAL PROTEIN MJ0182

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4331563_c2_172	1612	3532	1179	3540	181	1.2e-09

Protein name

Locus Name

Acc#

unknown

gp:AF011378

AF011378

Description

Bacteriophage sk1 complete genome.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4415938_c2_177	1613	3533	1627	4884	1863	3.4e-198

Protein name

Locus Name

Acc#

tail tip fiber protein gp21

pir:T13107

T13107

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4861263_c2_169	1614	3534	121	366		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4867819_c2_162	1615	3535	196	591	404	1.4e-37

Protein name

Locus Name

Acc#

hypothetical protein HP1334

pir:F64686

F64686

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5130075_c2_186	1616	3536	431	1296	858	1.1e-85

Protein name

Locus Name

Acc#

sp:DFP_HAEIN

P44953

Description

DNA/PANTOTHENATE METABOLISM FLAVOPROTEIN HOMOLOG

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
553437_f1_28	1617	3537	91	276		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6375032_c2_175	1618	3538	282	849	301	1.1e-33

Protein name

Locus Name

Acc#

minor tail protein gp19

pir:T13105

T13105

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
682777_c1_145	1619	3539	135	408		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
683187_c1_135	1620	3540	71	216		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6925452_f3_100	1621	3541	68	207	69	0.042

Protein name Locus Name Acc#

hypothetical protein APE0740 pir:E72664 E72664

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
790807_f1_16	1622	3542	101	306		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
830300_f1_21	1623	3543	65	198		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
865782_c3_198	1624	3544	750	2253	173	6.3e-12

Protein name

Locus Name

Acc#

gp:AB030825

AB030825

Description

Pseudomonas aeruginosa genomic DNA, partial sequence, strain:PAO1.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14175056_f1_2	1625	3545	67	204	116	4.5e-07

Protein name

Locus Name

Acc#

gp:ABCARRA

X70360

Description

A.brasilense carR gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23831527_c3_33	1626	3546	674	2025	619	1.7e-74

Protein name

Locus Name

Acc#

protein-disulfide reductase

gp:AF010322

AF010322

Description

Pseudomonas aeruginosa protein-disulfide reductase (dipZ) and catabolic dehydroquinase (aroQ) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26276961_c2_28	1627	3547	405	1218	1607	4.5e-165

Protein name

Locus Name

Acc#

chloroacetaldehyde dehydrogenase

gp:AF029733

AF029733

Description

Xanthobacter autotrophicus linear plasmid pXA01
chloroacetaldehyde dehydrogenase (aldA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33581289_c2_24	1628	3548	512	1539	1211	4.1e-123

Protein name

Locus Name

Acc#

sp:Y736_HAEIN

P44849

Description

HYPOTHETICAL SODIUM-DEPENDENT TRANSPORTER HI0736

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5312692_f3_15	1629	3549	411	1236	1075	1.1e-108

Protein name

sodium/proton-dependent alanine carrier pr
homolog yrbD

Locus Name

pir:C69972

Acc#

C69972

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6152307_c2_26	1630	3550	387	1164	1087	5.7e-110

Protein name

Locus Name

sp:CYDB_ECOLI

Acc#

P11027

Description

BD-I OXIDASE SUBUNIT II)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
781461_c2_25	1631	3551	480	1443	1563	2.1e-160

Protein name

Locus Name

sp:CYDA_AZOVI

Acc#

Q09049

Description

CYTOCHROME D UBIQUINOL OXIDASE SUBUNIT I,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
125143_c1_36	1632	3552	82	249	137	5.7e-09

Protein name

probable enoyl-CoA hydratase

Locus Name

pir:G75557

Acc#

G75557

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12632255_c3_48	1633	3553	239	720	136	8.4e-06

Protein name

probable erythrocyte-binding protein MAEBL

Locus Name

pir:T09127

Acc#

T09127

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13064425_f1_6	1634	3554	160	483	569	4.4e-55

Protein name

Locus Name

Acc#

sp:HEM6_ECOLI

P36553

Description

(COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16692186_f2_20	1635	3555	158	477	166	2.3e-12

Protein name

Locus Name

Acc#

sp:CYCP_ALCSP

P00138

Description

CYTOCHROME C'

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
195277_f1_11	1636	3556	405	1218	491	8.2e-47

Protein name

Locus Name

Acc#

ORF396 protein

gp:PSDNGC

Z73914

Description

Pseudomonas stutzeri orf1175 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
197137_c2_46	1637	3557	710	2133	965	2.5e-156

Protein name

Locus Name

Acc#

sp:DXS_HAEIN

P45205

Description

1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22697263_c1_37	1638	3558	104	315	87	0.0022

Protein name

Locus Name

Acc#

probable enoyl-coA hydratase

pir:E70868

E70868

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24323500_f1_5	1639	3559	171	516	435	7.0e-41

Protein name

Locus Name

Acc#

sp:HEM6_ECOLI

P36553

Description

(COPROPORPHYRINOGENASE) (COPROGEN OXIDASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30120325_c1_32	1640	3560	103	312		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33449042_c3_54	1641	3561	126	378	294	6.2e-26

Protein name

Locus Name

Acc#

SuhB

gp:AF010139

AF010139

Description

Azotobacter vinelandii iron-sulfur cluster assembly gene cluster, suhB, cysE2, iscS, iscU, iscA, hscB, hscA and fdx genes completedcds; ndk gene, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33986312_f2_16	1642	3562	209	630	522	4.3e-50

Protein name

Locus Name

Acc#

sp:GCH2_HAEIN

P44571

Description

GTP CYCLOHYDROLASE II,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35441086_c2_43	1643	3563	149	450	96	0.011

Protein name

Locus Name

Acc#

cell wall-binding protein homolog yvce

pir:F70031

F70031

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5859703_c1_33	1644	3564	464	1395	705	1.7e-69

Protein name

Locus Name

Acc#

gp:ECOFOLC

J02808

Description

E.coli folC gene encoding folylpolyglutamate-dihydrofolatesynthetase, and a protein required for its expression, completedcds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1046926_c1_177	1645	3565	217	654	325	3.2e-29

Protein name

Locus Name

Acc#

yrp protein:multiple regulator protein

pir:S70842

S70842

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10588311_c3_274	1646	3566	401	1206	1495	3.3e-153

Protein name

Locus Name

Acc#

ribonucleoside-diphosphate reductase, beta chain

pir:C64135

C64135

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10602250_f2_95	1647	3567	132	399	251	2.2e-21

Protein name

Locus Name

Acc#

aluminum tolerance protein

pir:PC4440

PC4440:PC4
514

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10751006_c1_182	1648	3568	153	462	125	5.0e-08

Protein name

Locus Name

Acc#

gp:ABCARRA

X70360

Description

A.brasilense carR gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11912951_f1_20	1649	3569	107	324		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1297216_c3_289	1650	3570	185	558	125	5.0e-08

Protein name

Locus Name

Acc#

colicin V production protein homolog

pir:E70195

E70195

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14275330_f2_68	1651	3571	489	1470	377	9.9e-35

Protein name

Locus Name

Acc#

sp:Y4WB_RHISN

P55680

Description

HYPOTHETICAL ZINC PROTEASE-LIKE PROTEIN Y4WB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14508500_c2_247	1652	3572	513	1542	1546	1.3e-158

Protein name

Locus Name

Acc#

amidophosphoribosyltransferase,

pir:XQEC

Description

F65003:A92

366:A92367

:S01389:I5

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14900187_f3_134	1653	3573	220	663	361	4.9e-33

Protein name

Locus Name

Acc#

probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase b1180

pir:A64864

A64864

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15908263_c1_143	1654	3574	108	327	307	2.6e-27

Protein name

RpsA

Locus Name

gp:AF035937

Acc#

AF035937

Description

Pseudomonas aeruginosa strain IATS O6 RpsA (rpsA) gene, partialcds; Ihf-Beta, Wzz (wzz), and Wzx (wzx) genes, complete cds; andwbp gene cluster for O-antigen biosynthesis, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16194442_f3_135	1655	3575	458	1377	1285	6.0e-131

Protein name

Locus Name

sp:PUR2_SALTY

Acc#

P26977

Description

RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16828790_f1_43	1656	3576	292	879	398	5.9e-37

Protein name

Locus Name

sp:YJAD_HAEIN

Acc#

P44710

Description

HYPOTHETICAL PROTEIN HI0432

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19698381_c1_189	1657	3577	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1972931_f2_63	1658	3578	68	207	57	0.023

Protein name

unknown

Locus Name

gp:AF197128

Acc#

AF197128

Description

Rattus norvegicus unknown mRNA.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20601558_c1_163	1659	3579	273	822	737	7.0e-73

Protein name

Locus Name

Acc#

sp:YGHU_ECOLI

Q46845

Description

HYPOTHETICAL 34.2 KD PROTEIN IN GSP-HYBG INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2111556_c1_164	1660	3580	1383	4152	161	1.3e-29

Protein name

Locus Name

Acc#

sp:EX5C_HAEIN

P44945

Description

EXODEOXYRIBONUCLEASE V GAMMA CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21642556_c3_272	1661	3581	87	264		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22751387_c3_271	1662	3582	150	453		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23611527_c3_275	1663	3583	114	345	140	1.3e-09

Protein name

Locus Name

Acc#

sp:YFAE_HAEIN

P45154

Description

HYPOTHETICAL PROTEIN H11309

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23676035_c3_262	1664	3584	410	1233	177	1.3e-10

Protein name

YtfP

Locus Name

gp:AF008220

Acc#

AF008220

Description

Bacillus subtilis rrnB-dnaB genomic region.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23725387_c2_244	1665	3585	318	957	1046	1.3e-105

Protein name

Locus Name

sp:FTSY_HAEIN

Acc#

P44870

Description

CELL DIVISION PROTEIN FTSY

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23728465_c1_161	1666	3586	925	2778	2856	2.0e-297

Protein name

pyruvate dehydrogenase (lipoamide)

Locus Name

gp:AZPDHE

Acc#

Y15124

Description

Azotobacter vinelandii pdhE gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23989512_c3_268	1667	3587	393	1182	1066	9.6e-108

Protein name

Locus Name

sp:PHEA_PSEST

Acc#

P27603

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24303127_c1_171	1668	3588	407	1224	797	3.1e-79

Protein name

carboxynorspermidine decarboxylase

Locus Name

gp:VIBCANSDC

Acc#

D31783

Description

Vibrio alginolyticus nspC gene for carboxynorspermidinedecarboxylase(CANS DC), complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24407750_c3_253	1669	3589	248	747	603	1.1e-58

Protein name

Locus Name

Acc#

sp:DCOP_HAEIN

P43812

Description

DECARBOXYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24642711_c2_216	1670	3590	773	2322	960	1.6e-96

Protein name

Locus Name

Acc#

sp:AROA_BACSU

P20691

Description

(5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25025987_c2_232	1671	3591	207	624	484	4.5e-46

Protein name

Locus Name

Acc#

sp:YRBH_ECOLI

P45395

Description

HYPOTHETICAL 35.2 KD PROTEIN IN MURA-RPON INTERGENIC REGION (O328)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25431625_c3_251	1672	3592	106	321	224	1.6e-18

Protein name

Locus Name

Acc#

sp:IHFB_ERWCH

P37983

Description

INTEGRATION HOST FACTOR BETA-SUBUNIT (IHFB-BETA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25445452_c1_144	1673	3593	215	648	313	6.0e-28

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:F75285

F75285

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30173201_f2_94	1679	3599	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30469092_c1_151	1680	3600	250	753	152	6.4e-09

Protein name

Locus Name

Acc#

unknown

gp:MLCL622

Z95398

Description

Mycobacterium leprae cosmid L622.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30600453_f3_139	1681	3601	697	2094	777	2.0e-86

Protein name

Locus Name

Acc#

hypothetical protein b2324

pir:B65005

B65005

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30720027_f3_141	1682	3602	154	465	382	2.9e-35

Protein name

Locus Name

Acc#

hypothetical protein

gp:PPPAL1

X74218

Description

Pseudomonas putida ruvB, tolQ, tolR, tolA, tolB and oprL genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31800280_c1_158	1683	3603	305	918	649	1.5e-63

Protein name

Locus Name

Acc#

hypothetical protein

gp:PFFC2

Y11998

Description

P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open readingframes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31828211_f2_69	1684	3604	1208	3627	2934	0.0

Protein name

proline dehydrogenase

Locus Name

gp:ATU39263

Acc#

U39263

Description

Agrobacterium tumefaciens plasmid pAtR10 proline dehydrogenase(putA) and Prp (prp) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33229667_c3_270	1685	3605	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33985930_f1_23	1686	3606	288	867		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34062503_c1_178	1687	3607	181	546	224	1.6e-18

Protein name

Locus Name

Acc#

sp:YHBN_HAEIN

P45074

Description

HYPOTHETICAL PROTEIN HI1149 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34172883_c1_176	1688	3608	166	501	296	3.8e-26

Protein name

Locus Name

Acc#

sp:YJEE_HAEIN

P44492

Description

HYPOTHETICAL PROTEIN HI0065 PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34409658_f2_84	1689	3609	360	1083	757	5.3e-75

Protein name

carboxyl esterase

Locus Name

pir:S57530

Acc#

S57530

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35157165_c1_191	1690	3610	204	615	303	2.7e-29

Protein name

methylated-DNA--protein-cysteine
S-methyltransferase, '

Locus Name

pir:D64604

Acc#

D64604

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36072135_c3_295	1691	3611	686	2061	564	1.5e-54

Protein name

Locus Name

sp:EX5A_ECOLI

Acc#

P04993:Q59
378

Description

ALPHA CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36112900_f2_91	1692	3612	103	312	253	1.4e-21

Protein name

Locus Name

gp:ECU24202

Acc#

U24202

Description

Escherichia coli ECOR 50 (yciD) gene, partial cds, and (yciC), (yciB), (yciA), membrane protein (tonB), (yciI), putative potassiumchannel (kch), and cardiolipin synthase (cls) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36129676_c3_252	1693	3613	139	420	85	0.00086

Protein name

hypothetical protein yrvD

Locus Name

pir:G69980

Acc#

G69980

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3915943_c2_226	1694	3614	414	1245	1163	5.0e-118

Protein name

Locus Name

Acc#

sp:METZ_PSEAE

P55218

Description

O-SUCCINYLMOMOSERINE SULFHYDRYLASE, (OSH SULFHYDRYLASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3922193_f2_50	1695	3615	381	1146	708	8.3e-70

Protein name

Locus Name

Acc#

probable pvdS protein

pir:B70591

B70591

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3933437_c2_229	1696	3616	202	609	387	8.6e-36

Protein name

Locus Name

Acc#

hypothetical protein jhp0867

pir:B71879

B71879

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4016943_f2_67	1697	3617	473	1422	653	5.6e-64

Protein name

Locus Name

Acc#

sp:Y4WA_RHISN

P55679

Description

HYPOTHETICAL ZINC PROTEASE Y4WA,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4103293_c1_179	1698	3618	245	738	822	6.9e-82

Protein name

Locus Name

Acc#

putative ABC transporter ATP-binding protein

gp:AF013987

AF013987

Description

Vibrio cholerae strain 0395 putative ABC transporter ATP-binding protein, sigma54 (rpoN), putative sigma54 modulation protein and nitrogen regulatory IIA protein (ptsN) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4114702_c1_159	1699	3619	119	360	194	2.4e-15

Protein name

probable dihydroneopterin aldolase,

Locus Name

pir:H65093

Acc#

H65093

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4489463_f2_90	1700	3620	425	1278		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4689693_c3_278	1701	3621	372	1119	509	8.2e-55

Protein name

Locus Name

Acc#

sp:MIAA_HAEIN

P44495

Description

(IPP TRANSFERASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4772050_f2_86	1702	3622	441	1326	487	2.2e-46

Protein name

Locus Name

Acc#

sp:DP3E_HAEIN

P43745

Description

DNA POLYMERASE III, EPSILON CHAIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4816513_c3_294	1703	3623	1318	3957	230	3.1e-41

Protein name

Locus Name

Acc#

sp:EX5B_ECOLI

P08394

Description

BETA CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4863458_c2_234	1704	3624	172	519		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4876525_c3_293	1705	3625	229	690		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4878135_c2_250	1706	3626	350	1053	810	1.3e-80

Protein name

Locus Name

Acc#

yhdG homolog

gp:AF040378

AF040378

Description

Serratia marcescens ribosomal protein L11 methyltransferase (prmA) gene, partial cds; and yhdG homolog and small DNA binding proteinFis (fis) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4881700_c3_290	1707	3627	479	1440	381	3.7e-35

Protein name

Locus Name

Acc#

hypothetical protein 5

pir:T00101

T00101

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4884675_c3_283	1708	3628	253	762	138	1.5e-07

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF031940

AF031940

Description

Sinorhizobium meliloti alcohol dehydrogenase (adhA) gene, completecds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5086693_c3_277	1709	3629	419	1260	793	8.2e-79

Protein name

hypothetical protein slr0049

Locus Name

pir:S74347

Acc#

S74347

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5098937_f2_51	1710	3630	543	1632	520	3.1e-53

Protein name

probable exodeoxyribonuclease VII large subunit

Locus Name

pir:C75549

Acc#

C75549

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5110963_c1_162	1711	3631	559	1680	1056	1.1e-106

Protein name

Locus Name

sp:ODP2_PSEAE

Acc#

Q59638

Description

COMPLEX, (E2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5112763_f2_89	1712	3632	277	834	364	2.4e-33

Protein name

Locus Name

sp:YDGM_HAEIN

Acc#

P71396

Description

PUTATIVE FERREDOXIN-LIKE PROTEIN HI1684

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5323750_f3_108	1713	3633	104	315		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
6484691_f1_26	1714	3634	377	1134	738	5.5e-73

Protein name

Locus Name

Acc#

sp:CYSP_ECOLI

P16700

Description

THIOSULFATE-BINDING PROTEIN PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
806512_c3_279	1715	3635	137	414	171	1.8e-12

Protein name

Locus Name

Acc#

polysialic acid capsule expression protein

pir:B70434

B70434

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
11562_c3_7	1716	3636	78	237		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
20395432_c2_6	1717	3637	70	213		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
36117135_f1_1	1718	3638	335	1008	1334	3.8e-136

Protein name

Locus Name

Acc#

malate dehydrogenase

gp:AF109682

AF109682

Description

Aquaspirillum arcticum malate dehydrogenase (MDH) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6682962_f1_2	1719	3639	85	258		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
13958403_f1_1	1720	3640	399	1200	1251	2.4e-127

Protein name

Locus Name

Acc#

sp:YLIG_ECOLI

P75802

Description

HYPOTHETICAL 49.6 KD PROTEIN IN MOEA-DACC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16506250_f2_4	1721	3641	140	423	236	4.8e-19

Protein name

Locus Name

Acc#

unknown

gp:AF026544

AF026544

Description

Ralstonia eutropha phbF and beta-ketothiolase (bktB) genes, complete cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20782550_f3_16	1722	3642	242	729	933	1.2e-93

Protein name

Locus Name

Acc#

sp:MTNG_NEIGO

P08455

Description

METHYLTRANSFERASE NGOP11) (M.NGOP11)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24328950_f2_8	1723	3643	153	462	336	2.2e-30

Protein name

Locus Name

Acc#

sp:YRFH_ECOLI

P45802

Description

HYPOTHETICAL 15.5 KD PROTEIN IN MRCA-PCKA INTERGENIC REGION (O133)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
29859790_c2_32	1724	3644	74	225		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
3942592_f2_6	1725	3645	252	759	741	2.6e-73

Protein name Locus Name Acc#

hypothetical protein, 26K pir:JC5479 JC5479

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4103390_f3_15	1726	3646	85	258	323	5.2e-29

Protein name Locus Name Acc#

sp:MTNG_NEIGO P08455

Description

METHYLTRANSFERASE NGOP11) (M.NGOP11)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
42837_f1_2	1727	3647	71	216	170	2.5e-12

Protein name Locus Name Acc#

sp:MTNG_NEIGO P08455

Description

METHYLTRANSFERASE NGOP11) (M.NGOP11)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
4976512_f2_7	1728	3648	518	1557	1265	7.8e-129

Protein name Locus Name Acc#

threonine dehydratase, biosynthetic pir:E75502 E75502

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7038307_f1_3	1729	3649	127	384	228	6.1e-19

Protein name

Locus Name

Acc#

sp:PA1F_HUMAN

Description

P24666:Q16

035:Q16725

(EC 3.1.3.48) (ADIPOCYTE ACID PHOSPHATASE, ISOZYME ALPHA)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30175950_f1_1	1730	3650	77	234	292	5.8e-25

Protein name

Locus Name

Acc#

sp:THIC_BACSU

Description

P45740:P71

090

THIAMINE BIOSYNTHESIS PROTEIN THIC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4470181_f3_5	1731	3651	156	471	635	4.5e-62

Protein name

Locus Name

Acc#

sp:THIC_ECOLI

P30136

Description

THIAMINE BIOSYNTHESIS PROTEIN THIC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7119001_f2_4	1732	3652	73	222	85	0.013

Protein name

Locus Name

Acc#

sp:YA51_HAEIN

Description

Q57180:O05

043

HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN HI1051

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24254702_f3_3	1733	3653	252	759	253	1.4e-21

Protein name

Locus Name

Acc#

sp:YIAT_ECOLI

P37681

Description

HYPOTHETICAL 27.4 KD PROTEIN IN AVTA-SELB INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25787500_c3_6	1734	3654	278	837	503	4.4e-48

Protein name

Locus Name

Acc#

sp:BFRA_NEIGO

P72080

Description

BACTERIOFERRITIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5133575_c3_7	1735	3655	162	489	489	1.3e-46

Protein name

Locus Name

Acc#

sp:BFRB_NEIGO

P77914

Description

BACTERIOFERRITIN B (BFR A) (BFR B)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21984375_c1_10	1736	3656	473	1422	708	8.3e-70

Protein name

Locus Name

Acc#

sp:AIP2_YEAST

P46681

Description

ACTIN INTERACTING PROTEIN 2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23535910_f1_2	1737	3657	492	1479	1489	1.4e-152

Protein name

Locus Name

Acc#

sp:YEQ_Q_ECOLI

P76403:008

007:008010

Description

PUTATIVE PROTEASE YEQ_Q,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25677176_f3_6	1738	3658	205	615	516	1.8e-49

Protein name

Locus Name

Acc#

site-specific DNA-methyltransferase
(cytosine-specific), HP1121

pir:A64660

A64660

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3926262_c2_13	1739	3659	225	678	134	8.6e-08

Protein name

TerZ

Locus Name

gp:AF168355

Acc#

AF168355

Description

Proteus mirabilis tellurite resistance locus, complete sequence;and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3946943_f1_1	1740	3660	510	1533	808	2.1e-80

Protein name

OprM

Locus Name

gp:AB011381

Acc#

AB011381

Description

Pseudomonas aeruginosa gene for OprM, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2110657_c2_3	1741	3661	221	663	570	3.5e-55

Protein name

Locus Name

sp:Y926_SYNY3

Acc#

P72872

Description

HYPOTHETICAL 37.9 KD PROTEIN SLL0926

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16040887_f3_11	1742	3662	504	1512	2557	9.6e-266

Protein name

unknown

Locus Name

gp:AF039312

Acc#

AF039312

Description

Moraxella catarrhalis strain 4223 transferrin binding protein A(tbpA) and transferrin binding protein B (tbpB) genes, completedcds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4016563_c1_13	1743	3663	108	327	92	0.00021

Protein name

conserved hypothetical protein ykoJ

Locus Name

pir:F69859

Acc#

F69859

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4484567_f1_1	1744	3664	899	2700	4565	0.0

Protein name

transferrin binding protein A

Locus Name

gp:AF039312

Acc#

AF039312

Description

Moraxella catarrhalis strain 4223 transferrin binding protein A (tbpA) and transferrin binding protein B (tbpB) genes, completecds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4775207_f2_9	1745	3665	173	522	728	1.6e-71

Protein name

transferrin binding protein A

Locus Name

gp:AF039315

Acc#

AF039315

Description

Moraxella catarrhalis strain Q8 transferrin binding protein A (tbpA) and transferrin binding protein B (tbpB) genes, completecds; and unknown gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33380275_f1_2	1746	3666	65	198		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35361043_c1_7	1747	3667	62	189	93	0.00048

Protein name

phosphate-binding protein,
phosphate-repressible

Locus Name

pir:I64120

Acc#

I64120

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36501561_c3_9	1748	3668	301	903	842	5.2e-84

Protein name

Locus Name

Acc#

sp:PSTC_HAEIN

P45191

Description

PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN PSTC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5960433_c1_8	1749	3669	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4429510_f1_1	1750	3670	477	1434	1328	1.7e-135

Protein name

Locus Name

Acc#

sp:MANB_SALMO

Q01411

Description

PHOSPHOMANNOMUTASE, (PMM)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4459376_c2_15	1751	3671	294	885	575	1.0e-55

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:D75311

D75311

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10429517_c1_34	1752	3672	413	1242	573	1.7e-55

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:A75525

A75525

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12384625_c3_48	1753	3673	362	1089	386	1.1e-35

Protein name

Locus Name

Acc#

sp:YGBO_ECOLI

Q57261

Description

HYPOTHETICAL 39.1 KD PROTEIN IN SURE-CYSC INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15915625_f2_13	1754	3674	170	513		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21673425_f2_12	1755	3675	447	1344	507	1.7e-48

Protein name

Locus Name

Acc#

sp:UBIH_ECOLI

P25534

Description

UBIH PROTEIN,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2195931_c1_29	1756	3676	69	210	93	0.0018

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_2107

pir:F70480

F70480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22355001_f3_23	1757	3677	73	222		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23954035_c3_50	1758	3678	175	528	119	3.8e-05

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_2107

pir:F70480

F70480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25665885_c2_36	1759	3679	241	726	389	6.3e-45

Protein name

Locus Name

Acc#

sp:MIAE_SALTY

Q08015

Description

TRNA- (MS[2

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30100880_c3_51	1760	3680	201	606	186	1.7e-14

Protein name

Locus Name

Acc#

hypothetical protein aq_2108

pir:G70480

G70480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3994052_f1_3	1761	3681	192	579	682	4.7e-67

Protein name

Locus Name

Acc#

probable dctp deaminase

pir:B71565

B71565

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4109790_c1_28	1762	3682	155	468	176	2.2e-12

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_2107

pir:F70480

F70480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4319837_c2_37	1763	3683	493	1482	466	3.7e-44

Protein name

Locus Name

Acc#

sp:YJEF_ECOLI

P31806

Description

HYPOTHETICAL 54.7 KD PROTEIN IN PSD-AMIB INTERGENIC REGION (URF1)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4345068_f3_21	1764	3684	128	387	177	1.5e-13

Protein name

Locus Name

Acc#

sp:YOHJ_ECOLI

P33372

Description

HYPOTHETICAL 14.6 KD PROTEIN IN PBPG-CDD INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4790637_f3_22	1765	3685	183	552	295	4.8e-26

Protein name

Locus Name

Acc#

sp:YOHK_HAEIN

P45146

Description

HYPOTHETICAL PROTEIN HI1298

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5900203_f1_1	1766	3686	689	2070	1609	2.8e-165

Protein name

Locus Name

Acc#

sp:REP_ECOLI

P09980

Description

ATP-DEPENDENT DNA HELICASE REP,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6658527_c2_39	1767	3687	184	555	228	5.6e-18

Protein name

Locus Name

Acc#

conserved hypothetical protein aq_2107

pir:F70480

F70480

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7226518_f2_17	1768	3688	102	309	112	1.2e-06

Protein name

Locus Name

Acc#

hypothetical protein

gp:POL010393

AJ010393

Description

Pseudomonas oleovorans phaI and phaF genes, and ORF1, ORF2(partial) and ORF3.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22897332_c2_15	1769	3689	153	462	338	1.3e-30

Protein name

Locus Name

Acc#

sp:FMAH_BACNO

P04953

Description

SUBUNITS PILIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36210875_f2_3	1770	3690	883	2652	3272	0.0

Protein name

Locus Name

Acc#

sp:ACO2_ECOLI

P36683:P36

648:Q59382

:P75652

Description

(ACONITASE 2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14853143_c1_9	1771	3691	703	2112	1460	1.7e-149

Protein name

Locus Name

Acc#

sp:YHGF_NEIME

Q51152

Description

HYPOTHETICAL 83.1 KD PROTEIN IN REGION E

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16050817_f1_1	1772	3692	225	678	203	2.7e-16

Protein name

Locus Name

Acc#

hypothetical protein sll0788

pir:S77018

S77018

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10175877_f3_73	1773	3693	264	795	124	2.2e-11

Protein name

Locus Name

Acc#

DnrD protein

gp:PST131715

AJ131715

Description

Pseudomonas stutzeri dnrD gene and ORF194 (partial) and ORF63(partial).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10195250_f2_49	1774	3694	81	246		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
10546930_f1_18	1775	3695	239	720	576	8.1e-56

Protein name

Locus Name

Acc#

sp:MODB_HAEIN

P45322

Description

MOLYBDENUM TRANSPORT SYSTEM PERMEASE PROTEIN MODB

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
11113152_f3_70	1776	3696	142	429	205	1.7e-16

Protein name

Locus Name

Acc#

hypothetical protein APE1291

pir:D72603

D72603

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12367711_f3_63	1777	3697	259	780	438	3.4e-41

Protein name

Locus Name

Acc#

sp:MODD_AZ0VI

P37732

Description

MOLYBDENUM TRANSPORT ATP-BINDING PROTEIN MODD

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15710327_c1_84	1778	3698	266	801	427	5.0e-40

Protein name

Locus Name

Acc#

putative chaperone

gp:PSNARXL

Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15781576_c2_103	1779	3699	223	672	594	1.0e-57

Protein name

Locus Name

Acc#

sp:YADF_ECOLI

Description

P36857:P75
656

HYPOTHETICAL 25.1 KD PROTEIN IN HPT-PAND INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19735188_f3_58	1780	3700	677	2034	484	3.8e-70

Protein name

Locus Name

Acc#

nitrate/nitrite sensory protein

gp:PSNARXL

Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19806552_f2_31	1781	3701	187	564	134	5.5e-08

Protein name

Locus Name

Acc#

Notch homolog

gp:AF033013

AF033013

Description

Bombyx mori Notch homolog mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19806552_f3_51	1782	3702	180	543	142	1.3e-09

Protein name

Locus Name

Acc#

Notch homolog

gp:AF033013

AF033013

Description

Bombyx mori Notch homolog mRNA, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20423500_f2_33	1783	3703	269	810	420	2.7e-39

Protein name

Locus Name

Acc#

sp:MOEB_SALTY

Q56067

Description

MOLYBDOPTERIN BIOSYNTHESIS MOEB PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20587686_f1_8	1784	3704	139	420		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
20876387_f1_13	1785	3705	234	705	247	5.9e-21

Protein name

Locus Name

Acc#

sp:YIIM_ECOLI

P32157

Description

HYPOTHETICAL 26.6 KD PROTEIN IN KDGT-CPXA INTERGENIC REGION (O234)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21485962_c2_129	1786	3706	63	189		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21673452_c3_141	1787	3707	448	1347	1455	5.8e-149

Protein name

Locus Name

Acc#

nitrate extrusion protein

gp:PSNARXL

Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21688888_c1_76	1788	3708	332	999	1035	1.8e-104

Protein name

Locus Name

Acc#

sp:THII_SALTY

P55913:006
955

Description

THIAMINE BIOSYNTHESIS PROTEIN THII

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22000717_f1_19	1789	3709	145	438		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22378418_f1_17	1790	3710	283	852	502	5.6e-48

Protein name Locus Name Acc#

sp:MODA_HAEIN P45323

Description

MOLYBDATE-BINDING PERIPLASMIC PROTEIN PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22554031_f3_60	1791	3711	194	585	499	1.2e-47

Protein name Locus Name Acc#

sp:MOAB_ECOLI P30746

Description

MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN B

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24068812_f1_12	1792	3712	258	777	561	3.1e-54

Protein name Locus Name Acc#

nitrate/nitrite regulatory protein gp:PSNARXL Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24423375_f1_5	1793	3713	71	216		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24423375_f2_32	1794	3714	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24651536_f1_16	1795	3715	200	603	310	1.2e-27

Protein name

Locus Name

Acc#

sp:Y903_SYNY3

Q55371

Description

HYPOTHETICAL 16.5 KD PROTEIN SLR0903

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25507260_f1_9	1796	3716	338	1017	82	0.048

Protein name

Locus Name

Acc#

MHC class I antigen

pir:I57454

I57454

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
275283_f1_15	1797	3717	196	591	142	7.9e-10

Protein name

Locus Name

Acc#

hypothetical protein Rv2453c

pir:D70864

D70864

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2853437_f1_11	1798	3718	66	201		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29432768_c2_123	1799	3719	91	276		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30509827_f1_7	1800	3720	134	405		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31453162_c2_128	1801	3721	77	234	197	1.2e-15

Protein name

Locus Name

Acc#

hypothetical protein

gp:AF213822

AF213822

Description

Zymomonas mobilis strain ZM4 fosmid clone 42B3, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33331633_c1_83	1802	3722	521	1566	2362	4.4e-245

Protein name

Locus Name

Acc#

respiratory nitrate reductase beta subunit

gp:PSNARXL

Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33758515_f1_6	1803	3723	174	525		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36351552_f3_61	1804	3724	91	276	145	3.8e-10

Protein name

hypothetical protein ssr1527

Locus Name

pir:S75710

Acc#

S75710:S75
718

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36371012_c2_102	1805	3725	60	183		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
3906555_f2_36	1806	3726	172	519	296	3.8e-26

Protein name

probable molybdenum-pterin-binding-protein

Locus Name

pir:S57954

Acc#

S57954

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4011062_c1_91	1807	3727	427	1284	1152	7.4e-117

Protein name

nitrate extrusion protein

Locus Name

gp:PSNARXL

Acc#

Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4070308_c3_134	1808	3728	442	1329	676	2.0e-66

Protein name

Locus Name

Acc#

sp:MOEA_HAEIN

P45210

Description

MOLYBDOPTERIN BIOSYNTHESIS MOEA PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4344003_f3_59	1809	3729	364	1095	737	7.0e-73

Protein name

Locus Name

Acc#

sp:MOAA_HAEIN

P45311

Description

MOLYBDENUM COFACTOR BIOSYNTHESIS PROTEIN A

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4788876_c3_133	1810	3730	248	747	704	2.2e-69

Protein name

Locus Name

Acc#

respiratory nitrate reductase gamma subunit

gp:PSNARXL

Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4797093_f3_52	1811	3731	157	474		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4806502_c2_127	1812	3732	102	309	117	3.5e-07

Protein name

Locus Name

Acc#

negative regulator of translation

gp:AF213822

AF213822

Description

Zymomonas mobilis strain ZM4 fosmid clone 42B3, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4886251_f2_35	1813	3733	168	507	354	2.7e-32

Protein name molybdenum cofactor biosynthesis protein C Locus Name gp:AF108766 Acc# AF108766

Description

Rhodobacter sphaeroides AsmA (asma) gene, partial cds; YbaU (ybaU), anthranilate synthase component I (trpE), YibQ (yibQ), anthranilatesynthase component II (trpG), anthranilatephosphoribosyltransferase (trpD), indole-3-glycerol phosphatesynthase (trpC), molybdenum cofactor biosynthesis protein C (moaC), molybdenum cofactor biosynthesis protein A (moeA), LexA

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4897576_c3_147	1814	3734	69	210		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5282812_f3_56	1815	3735	65	198	52	0.032

Protein name MDP1 Locus Name gp:AB013441 Acc# AB013441

Description

Mycobacterium bovis gene for MDP1, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
630053_f2_47	1816	3736	385	1158	320	1.1e-28

Protein name ORF396 protein Locus Name gp:PSDNGC Acc# Z73914

Description

Pseudomonas stutzeri orf175 gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
635903_f1_10	1817	3737	75	228		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7064692_c1_86	1818	3738	369	1110	415	9.3e-39

Protein name Locus Name Acc#
 NifM protein gp:PSNARXL Y15252

Description

Pseudomonas aeruginosa narX, narL, narK1, narK2, narG, narH, narJ, narI, nifM, moaA genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7225637_f3_50	1819	3739	1739	5220	540	6.2e-50

Protein name Locus Name Acc#
 filamentous hemagglutinin-like protein pir:T09083 T09083
 PspA:probable secreted protein

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9814751_c3_131	1820	3740	1271	3816	5075	0.0

Protein name Locus Name Acc#
 alpha-subunit of nitrate reductase gp:PFU71398 U71398

Description

Pseudomonas fluorescens nitrate reductase alpha-subunit (narG) and beta-subunit (narH) genes, partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1176576_f3_28	1821	3741	157	474	314	4.7e-28

Protein name Locus Name Acc#
 sp:YAI1_ECOLI

Description

P52088:P75703

HYPOTHETICAL 17.0 KD PROTEIN IN PROC-AROL INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14647507_f2_20	1822	3742	405	1218	386	1.1e-35

Protein name Locus Name Acc#
 conserved hypothetical protein aq_740 pir:A70365 A70365

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23443752_f3_23	1823	3743	661	1986	298	3.4e-23

Protein name

Locus Name

Acc#

sp:YTRP_PSEPU

P40604

Description

HYPOTHETICAL 62.7 KD PROTEIN IN TRPE-TRPG INTERGENIC REGION PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
23610636_c3_58	1824	3744	274	825	755	8.7e-75

Protein name

Locus Name

Acc#

sp:YQCB_HAEIN

P44197

Description

HYPOTHETICAL PROTEIN HI1435

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
24644035_c2_45	1825	3745	219	660	255	8.4e-22

Protein name

Locus Name

Acc#

probable citrate lyase beta chain

pir:T35062

T35062

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
250251_f2_18	1826	3746	192	579	525	2.0e-50

Protein name

Locus Name

Acc#

sp:PUR6_HAEIN

P43849

Description

(EC 4.1.1.21) (AIR CARBOXYLASE) (AIRC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT Length</u>	<u>AA Length</u>	<u>Score</u>	<u>Probability</u>
25485763_f1_1	1827	3747	89	270		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25510974_c1_34	1828	3748	185	558	331	7.4e-30

Protein name

Locus Name

Acc#

sp:YBEQ_ECOLI

P77234

Description

HYPOTHETICAL 37.3 KD PROTEIN IN LEUS-GLTL INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
29304668_f3_30	1829	3749	302	909	556	1.1e-53

Protein name

Locus Name

Acc#

sp:SYK3_ECOLI

P03812:P78
141

Description

HYPOTHETICAL LYSYL-TRNA SYNTHETASE HOMOLOG, (GX)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31275301_f1_11	1830	3750	352	1059	516	1.8e-49

Protein name

Locus Name

Acc#

sp:PDXB_ECOLI

P05459

Description

ERYTHRONATE-4-PHOSPHATE DEHYDROGENASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34179211_f3_24	1831	3751	330	993	158	1.2e-08

Protein name

Locus Name

Acc#

probable protein serine-threonine
phosphatase

pir:C75297

C75297

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36365625_f2_17	1832	3752	147	444	348	1.2e-31

Protein name

Locus Name

Acc#

hypothetical protein jhp1377

pir:D71815

D71815

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5118952_c1_35	1833	3753	403	1212	703	2.8e-69

Protein name

Locus Name

Acc#

sp:PYR2_PSEAE

Q51551

Description

CATALYTIC CHAIN)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5275300_f3_22	1834	3754	347	1044	954	7.1e-96

Protein name

Locus Name

Acc#

sp:BI0B_ECOLI

P12996

Description

BIOTIN SYNTHASE, (BIOTIN SYNTHETASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
5948342_f3_27	1835	3755	259	780	530	6.0e-51

Protein name

Locus Name

Acc#

sp:PURK_PSEAE

P72158

Description

(AIR CARBOXYLASE) (AIRC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7041_f1_8	1836	3756	132	399	155	1.5e-10

Protein name

Locus Name

Acc#

sp:PURK_AQUAE

O66608

Description

(AIR CARBOXYLASE) (AIRC)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12991392_f2_18	1837	3757	101	306	160	9.7e-12

Protein name

Locus Name

Acc#

unknown

gp:PDU08856

U08856

Description

Paracoccus denitrificans insertion sequence IS1248b, complete sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15110912_c3_69	1838	3758	358	1077	690	6.7e-68

Protein name

Locus Name

Acc#

sp:YQJM_BACSU

P54550

Description

PROBABLE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE YQJM,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15632781_c2_61	1839	3759	79	240		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
15673816_f3_31	1840	3760	472	1419	1772	1.5e-182

Protein name

Locus Name

Acc#

type I site-specific deoxyribonuclease, Hsd
chain R:type I restriction enzyme, Hsd, chain
R:type I restriction-modification system,

pir:JC5216

JC5216

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19823578_f3_29	1841	3761	405	1218	130	1.0e-07

Protein name

Locus Name

Acc#

hypothetical protein

pir:A75592

A75592

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21642052_c3_70	1842	3762	232	699	686	1.8e-67

Protein name

Locus Name

Acc#

sp:YC78_HAEIN

Q57431:005
050

Description

POTATIVE NAD(P)H NITROREDUCTASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21673201_f3_25	1843	3763	220	663	364	2.4e-33

Protein name

protein Tp70

Locus Name

pir:A71309

Acc#

A71309:S18

231:S19826

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2189075_c2_66	1844	3764	126	381	195	1.9e-15

Protein name

Locus Name

sp:YPRO_OWEFU

Acc#

P21260:P21

261

Description

HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22143752_f1_9	1845	3765	636	1911	2756	7.9e-287

Protein name

type I site-specific deoxyribonuclease, Hsd
chain R:type I restriction enzyme, Hsd, chain
R:type I restriction-modification system,

Locus Name

pir:JC5216

Acc#

JC5216

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23437551_f1_4	1846	3766	83	252		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23490937_c3_81	1847	3767	93	282	73	0.037

Protein name

nicotinamide adenine dinucleotide
dehydrogenase

Locus Name

gp:AF025836

Acc#

AF025836

Description

Echinostoma sp.I. Africa nicotinamide adenine dinucleotidedehydrogenase
subunit 1 (ND1) gene, mitochondrial gene encodingmitochondrial protein,
partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24704462_c2_51	1848	3768	206	621	296	3.8e-26

Protein name

cinnamyl-alcohol dehydrogenase

Locus Name

gp:AF083333

Acc#

AF083333

Description

Medicago sativa cinnamyl-alcohol dehydrogenase (MsaCad1) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
32667715_f3_26	1849	3769	188	567	106	0.00093

Protein name

hypothetical protein TP0570

Locus Name

pir:H71308

Acc#

H71308

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
35350802_f1_5	1850	3770	167	504	345	2.4e-31

Protein name

putative transposase

Locus Name

gp:AF007429

Acc#

AF007429

Description

Haemophilus paragallinarum IS-like putative transposase gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
36564842_f2_19	1851	3771	460	1383	573	1.7e-55

Protein name

type I site-specific deoxyribonuclease, Hsd
chain S:type I restriction enzyme, Hsd, chain
S:type I restriction-modification system,

Locus Name

pir:JC5218

Acc#

JC5218

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4032715_f3_27	1852	3772	116	351	214	1.8e-17

Protein name

Locus Name

sp:Y4SN_RHISN

Acc#

P50358

Description

HYPOTHETICAL 14.4 KD PROTEIN Y4SN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4111333_f3_33	1853	3773	201	603	238	5.3e-20

Protein name

Locus Name

Acc#

sp:NAHR_PSEPU

P10183

Description

TRANSCRIPTIONAL ACTIVATOR PROTEIN NAHR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4895127_c1_36	1854	3774	116	351	334	3.6e-30

Protein name

Locus Name

Acc#

Orf8

gp:AB011413

AB011413

Description

Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7034808_c1_49	1855	3775	70	213	51	0.033

Protein name

Locus Name

Acc#

hypothetical protein ZK856.5

pir:T28044

T28044

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7080001_f1_2	1856	3776	371	1116	298	2.3e-26

Protein name

Locus Name

Acc#

sp:YGCG_ECOLI

P55140

Description

HYPOTHETICAL 34.9 KD PROTEIN IN CYSJ-ENO INTERGENIC REGION (O313)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7083578_c1_37	1857	3777	60	183	162	2.4e-11

Protein name

Locus Name

Acc#

NADP-dependent alcohol hydrogenase

gp:LMFL1063

AL121862

Description

Leishmania major Friedlin chromosome 23 cosmid L1063, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
9782666_f1_7	1858	3778	554	1665	2520	8.0e-262

Protein name

ALXA and HSDM

Locus Name

gp:PHU46781

Acc#

U46781

Description

Pasteurella haemolytica putative coproporphyrinogen III oxidase(hemN') gene, partial cds, leukotoxin transcriptional activator and restriction modification methylase subunit (alxA-hsdM), (hsdS) and (hsdR) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14257160_f1_2	1859	3779	294	885		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16180437_f3_18	1860	3780	502	1509	1460	1.7e-149

Protein name

Locus Name

Acc#

sp:GABD_ECOLI

P25526

Description

, (SSDH)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19806552_f1_1	1861	3781	174	525	131	2.6e-07

Protein name

probable ankyrin

Locus Name

pir:H71274

Acc#

H71274

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24407502_f3_17	1862	3782	224	675	392	2.5e-36

Protein name

glycine betaine/carnitine/choline ABC transporter (membrane p) opuCD

Locus Name

pir:F69670

Acc#

F69670

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25900252_c2_30	1863	3783	417	1254	138	1.3e-05

Protein name

putative natural resistance-associated

Locus Name

gp:CCA133735

Acc#

AJ133735

Description

Cyprinus carpio mRNA for putative natural resistance-associated macrophage protein (NRAMP).

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34094385_c1_23	1864	3784	107	324	155	6.3e-11

Protein name

AttJ

Locus Name

gp:U59485

Acc#

U59485:L63
540

Description

Agrobacterium tumefaciens AtrC (atrC) gene, partial cds; AtrB (atrB), AtrA (atrA), AttA1 (attA1), AttA2 (attA2), AttB (attB), AttC (attC), AttD (attD), AttE (attE), and AttF (attF) genes, complete cds; AttG (attG) gene, alternative splice products, complete cds; AttH (attH), AttI (attI), AttJ (attJ), AttK (attK), AttL (attL), AttM (attM), AttO (attO), AttP (attP), AttR (attR), AttS (attS), AttT (attT), AttU (attU), attV (attV), AttW (attW), AttX

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4770887_f1_3	1865	3785	176	531	130	2.7e-14

Protein name

hypothetical protein

Locus Name

gp:SSU18930

Acc#

Y18930

Description

Sulfolobus solfataricus 281 kb genomic DNA fragment, strain P2.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4875260_c2_33	1866	3786	72	219		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4884702_c1_27	1867	3787	226	681	404	1.4e-37

Protein name

NonF

Locus Name

gp:AF074603

Acc#

AF074603

Description

Streptomyces griseus subsp. griseus nonactin biosynthesis genecluster, partial sequence.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6740692_f2_10	1868	3788	165	498		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
7218752_f3_15	1869	3789	129	390	88	0.030

Protein name

putative polysaccharide polymerase

Locus Name

gp:SPCPS14E

Acc#

X85787

Description

S.pneumoniae cps14 locus.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
786305_f1_5	1870	3790	317	954	632	9.4e-62

Protein name

probable osmoprotection binding protein

Locus Name

pir:G71892

Acc#

G71892

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
792090_f2_12	1871	3791	148	447		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
12273437_f3_58	1872	3792	337	1014	1680	8.3e-173

Protein name

Locus Name

Acc#

sp:SYGA_MORCA

P77892

Description

ALPHA CHAIN) (GLYRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14181500_f2_36	1873	3793	693	2082	1593	1.4e-163

Protein name

Locus Name

Acc#

sp:SYGB_HAEIN

P43822

Description

BETA CHAIN) (GLYRS)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19650062_c1_101	1874	3794	279	840	581	2.4e-56

Protein name

Locus Name

Acc#

sp:BUDC_KLEPN

Q48436

Description

ACETOIN(DIACETYL) REDUCTASE, (ACETOIN DEHYDROGENASE) (AR)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21648382_f1_22	1875	3795	279	840	813	6.2e-81

Protein name

Locus Name

Acc#

sp:ACCA_ECOLI

P30867

Description

(EC 6.4.1.2)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21650017_c2_112	1876	3796	254	765	437	4.3e-41

Protein name

Locus Name

Acc#

sp:LPTP_ECOLI

P23885

Description

LEUCYL/PHENYLALANYL-TRNA--PROTEIN TRANSFERASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21657752_c3_147	1877	3797	345	1038	580	3.0e-56

Protein name

Locus Name

Acc#

sp:YZ37_SYNY3

Q55480

Description

HYPOTHETICAL SUGAR KINASE SLR0537

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21987811_f2_34	1878	3798	237	714	384	6.2e-41

Protein name

Locus Name

Acc#

sp:PGSA_HAEIN

P44528

Description

(EC 2.7.8.5) (PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE) (PGP SYNTHASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22038132_f3_67	1879	3799	76	231		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22384628_f1_5	1880	3800	448	1347	1005	2.8e-101

Protein name

Locus Name

Acc#

sp:YKGC_ECOLI

P77212

Description

INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23493812_f2_33	1881	3801	998	2997	972	6.2e-119

Protein name

Locus Name

Acc#

metalloprotease 1

gp:AF061243

AF061243

Description

Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23875027_f2_50	1882	3802	396	1191	621	1.4e-60

Protein name

Locus Name

Acc#

sp:RLUC_HAEIN

P44433

Description

(PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24118802_c3_138	1883	3803	441	1326	1742	2.2e-179

Protein name

Locus Name

Acc#

serine hydroxymethyltransferase

gp:AF073769

AF073769

Description

Acinetobacter radioresistens serine hydroxymethyltransferase (glyA) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24268777_c3_134	1884	3804	1181	3546	1542	1.5e-160

Protein name

Locus Name

Acc#

ribonuclease E, :cell shape-determining
protein:message stability-altering
protein:RNase E

pir:S27311

A64852:S45

572:S27311

:A23747:JG

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24900257_f1_11	1885	3805	86	261	145	3.8e-10

Protein name

Locus Name

Acc#

conserved hypothetical protein

pir:B72287

B72287

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
25657776_c1_102	1886	3806	149	450	180	7.4e-14

Protein name

Locus Name

Acc#

sp:PSPE_ECOLI

P23857

Description

PHAGE SHOCK PROTEIN E PRECURSOR

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26565686_c3_149	1887	3807	348	1047	691	5.2e-68

Protein name

hypothetical protein slr0787

Locus Name

pir:S77001

Acc#

S77001

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
26754011_c1_86	1888	3808	357	1074	1765	8.1e-182

Protein name

NAD repressor/NMN transporter NadRp

Locus Name

gp:MCU73324

Acc#

U73324

Description

Moraxella catarrhalis glycyl-tRNA synthetase beta subunit (GlyRS) and NAD repressor/NMN transporter NadRp (NadR) genes, partial cds, and glycyl-tRNA synthetase alpha subunit (GlyRS) gene, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
2845637_c3_137	1889	3809	172	519	168	1.4e-12

Protein name

Locus Name

sp:UBIC_ECOLI

Acc#

P26602:P76
783

Description

CHORISMATE--PYRUVATE LYASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30332811_f2_51	1890	3810	541	1626	1087	5.7e-110

Protein name

exopolyphosphatase

Locus Name

gp:AF053463

Acc#
AF053463

Description

Pseudomonas aeruginosa thioredoxin (trx) and exopolyphosphatase (ppx) genes, complete cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30726562_f3_62	1891	3811	768	2307	2256	7.6e-234

Protein name

hypothetical protein

Locus Name

gp:PFFC2

Acc#
Y11998

Description

P.fluorescens FC2.1, FC2.2, FC2.3c, FC2.4 and FC2.5c open readingframes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
33240686_c3_140	1892	3812	260	783	155	1.4e-09

Protein name

Locus Name

Acc#

sp:PNUC_ECOLI

Description

P31215:P77
227

PNUC PROTEIN

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34421878_c2_120	1893	3813	408	1227	991	8.5e-100

Protein name

Locus Name

Acc#

sp:YHIN_ECOLI

Description

P37631:P76
705

HYPOTHETICAL 43.8 KD PROTEIN IN RHSB-PIT INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
34578126_f3_54	1894	3814	355	1068	91	0.023

Protein name

Locus Name

Acc#

translation elongation factor eEF-1 alpha
chain PIK-A49:phosphatidylinositol 4-kinase
activator PIK-A49

pir:A45325

A45325:B45
325:C45325
:D45325:E4

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4695252_f2_29	1895	3815	213	642	497	1.9e-47

Protein name

Locus Name

Acc#

sp:YHGI_ECOLI

P46847

Description

HYPOTHETICAL 21.0 KD PROTEIN IN BIOH-GNTT INTERGENIC REGION (O191)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4875885_c2_126	1896	3816	164	495	120	1.7e-07

Protein name

Locus Name

Acc#

sp:YFMU_COXBU

P45680

Description

HYPOTHETICAL 15.8 KD PROTEIN IN FMU-RPMH INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6651712_f1_15	1897	3817	536	1611	1545	1.7e-158

Protein name

isocitrate lyase

Locus Name

gp:AB004651

Acc#

AB004651

Description

Hyphomicrobium methylovorum gene for isocitrate lyase, inorganic phosphate transporter, methionine synthase, complete and partial cds.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
6759625_c3_150	1898	3818	187	564	248	4.6e-21

Protein name

hypothetical protein TP0895

Locus Name

pir:D71266

Acc#

D71266

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14642925_f3_23	1899	3819	351	1056		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
16693750_f3_17	1900	3820	100	303	137	2.7e-09

Protein name

conserved hypothetical protein yerL

Locus Name

pir:A69795

Acc#

A69795

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
183437_f3_18	1901	3821	496	1491	2443	1.2e-253

Protein name

Locus Name

Acc#

sp:AMID_MORCA

Q49091

Description

POTATIVE AMIDASE,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
1987793_f2_16	1902	3822	264	795	189	8.2e-15

Protein name

Locus Name

Acc#

sp:MINC_ECOLI

P18196

Description

CELL DIVISION INHIBITOR MINC

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22078181_c3_52	1903	3823	137	411	161	7.6e-12

Protein name

Locus Name

Acc#

maf-type protein

pir:D72129

D72129

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22942053_f1_9	1904	3824	70	210		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
23492792_c2_37	1905	3825	203	612	141	1.0e-09

Protein name

Locus Name

Acc#

sp:CYC5_AZOVI

P11732

Description

CYTOCHROME C5

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24259651_f2_14	1906	3826	319	960	462	9.7e-44

Protein name

Locus Name

Acc#

sp:YIHG_ECOLI

P32129

Description

HYPOTHETICAL 36.3 KD PROTEIN IN DSBA-POLA INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
24351556_c1_28	1907	3827	231	696	389	5.3e-36

Protein name outer membrane protein homolog Locus Name gp:AF067083 Acc# AF067083

Description

Vitreoscilla sp. outer membrane protein homolog gene, complete cds;Trp repressor binding protein gene, partial cds; and unknown genes.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
30203430_c2_35	1908	3828	86	261		

Protein name Locus Name Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
31423200_f3_25	1909	3829	181	546	622	1.1e-60

Protein name Locus Name Acc#

cell division inhibitor minD:septum site-determining protein minD pir:CCECID B31877:D64 863

Description

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4729837_f3_19	1910	3830	317	954	1626	4.4e-167

Protein name Locus Name Acc#

BRO-1 gp:MCBLABRO1 Z54180

Description

M.catarrhalis bla gene.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
4791053_c1_31	1911	3831	72	219	54	0.0063

Protein name Locus Name Acc#

gag protein gp:MUSERVGG2 M26006

Description

Mouse endogenous retrovirus truncated gag gene, complete cds, cloned env-2 15.3.

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
976677_f3_20	1912	3832	494	1485	2124	7.4e-220

Protein name

Locus Name

Acc#

sp:YBL3_MORCA

Q49092

Description

HYPOTHETICAL 46.4 KD PROTEIN IN BLOR-1 3'REGION (ORF3)

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
14469635_f2_5	1913	3833	716	2151	1425	8.7e-146

Protein name

Locus Name

Acc#

sp:OPDA_HAEIN

P44573

Description

OLIGOPEPTIDASE A,

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
19569430_c3_39	1914	3834	275	828	454	6.8e-43

Protein name

Locus Name

Acc#

sp:YBHP_ECOLI

P75772

Description

HYPOTHETICAL 28.8 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
21718878_c1_20	1915	3835	269	810		

Protein name

Locus Name

Acc#

Description

NO-HIT

<u>ORF Name</u>	<u>NTID</u>	<u>AAID</u>	<u>NT</u> <u>Length</u>	<u>AA</u> <u>Length</u>	<u>Score</u>	<u>Probability</u>
22847175_f3_15	1916	3836	83	252	81	0.0023

Protein name

Locus Name

Acc#

sp:YHEV_ECOLI

P56622

Description

HYPOTHETICAL 7.6 KD PROTEIN IN SLYD-KEFB INTERGENIC REGION

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